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RDVER5.SEQ  ATGATGAAGCGTGAGAAAAATGTCATCTATGGCCCTGAGC 40
RD7.SEQ     ATGATGAAGCGTGAGAAAAATGTCATCTATGGCCCTGAGC 40
RDVER51.SEQ ATGATGAAGCGTGAGAAAAATGTCATCTATGGCCCTGAGC 40
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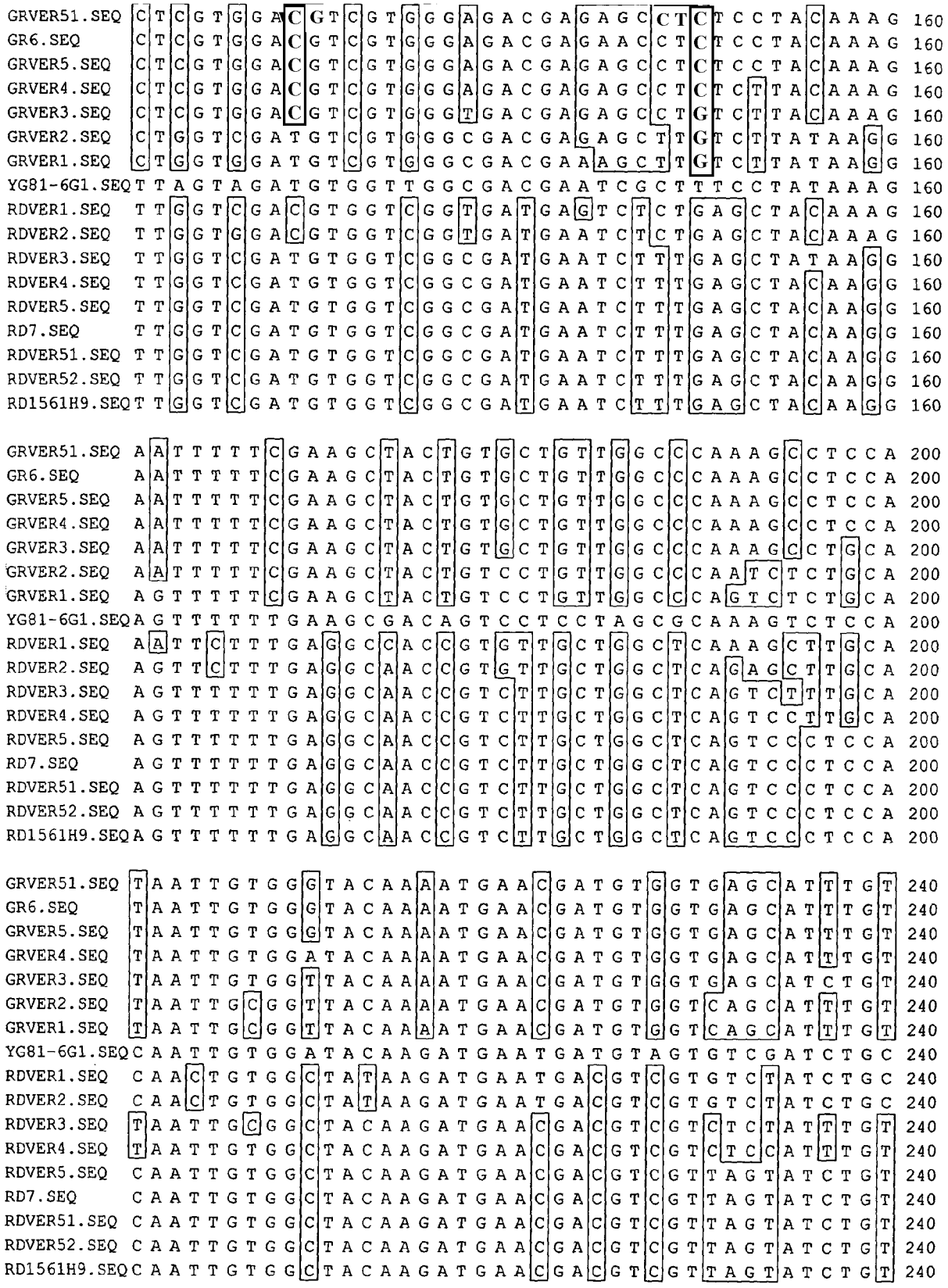
FIG. 2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GRVER4.SEQ TAATTGTGGATACAAAATGAACGATGTGGTGAGCATTTGT 240
GRVER3.SEQ TAATTGTGGTTACAAAATGAACGATGTGGTGAGCATCTGT 240
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GRVER1.SEQ TAATTGCGGTTACAAAATGAACGATGTGGTCAGCATTTGT 240
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RD7.SEQ CAATTGTGGCTACAAGATGAACGACGTCGTTAGTATCTGT 240
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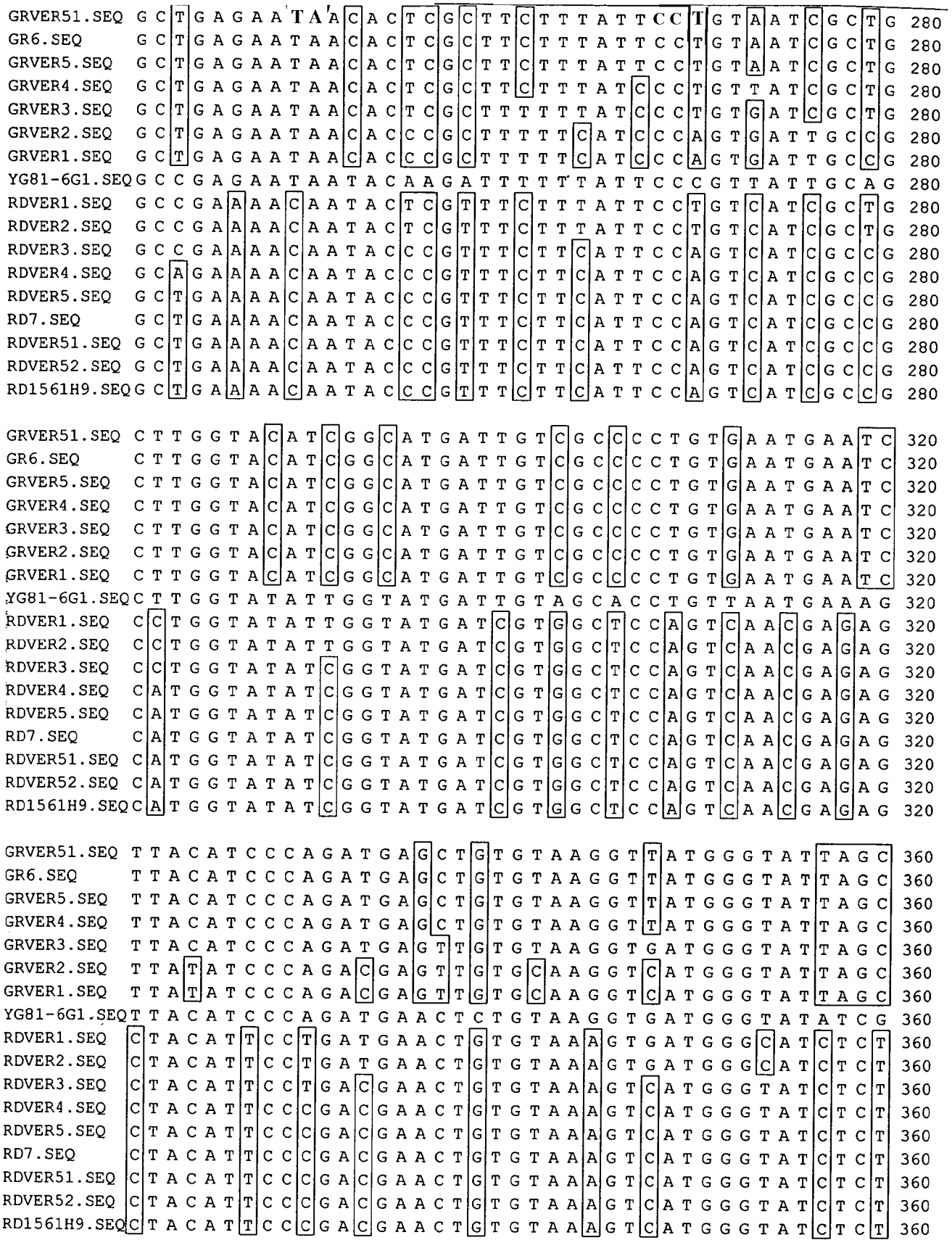
FIG. 2 (cont'd)



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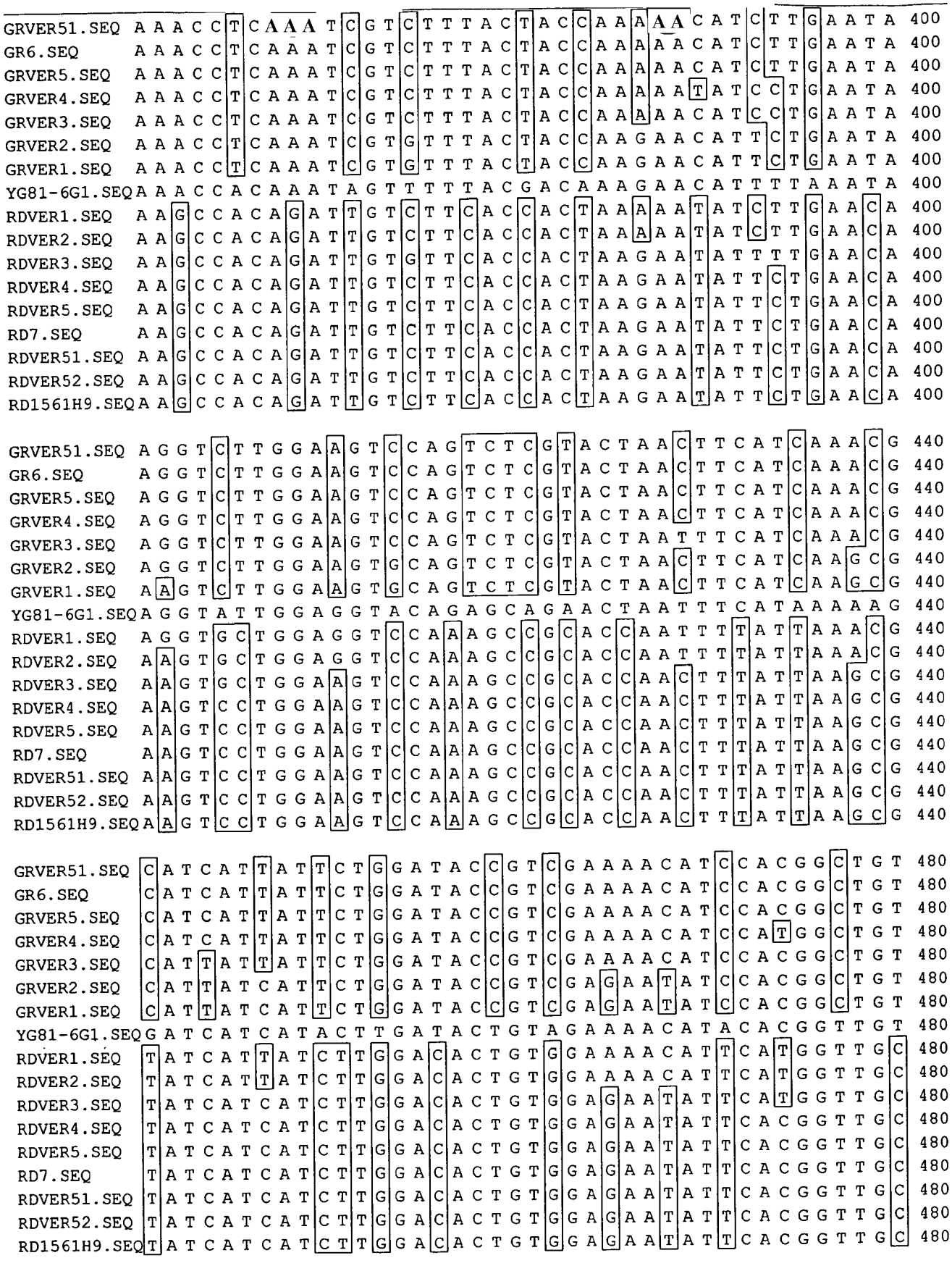
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GRVER1.SEQ AAGTCTTGGAAGTGCAGTCTCGTACTAACTTCATCAAGCG 440
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FIG. 2 (cont'd)

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GRVER4.SEQ   G A G A G C C T G C C T A A C T T C A T C T C T C G T T A C A G C G A T G G T A 520
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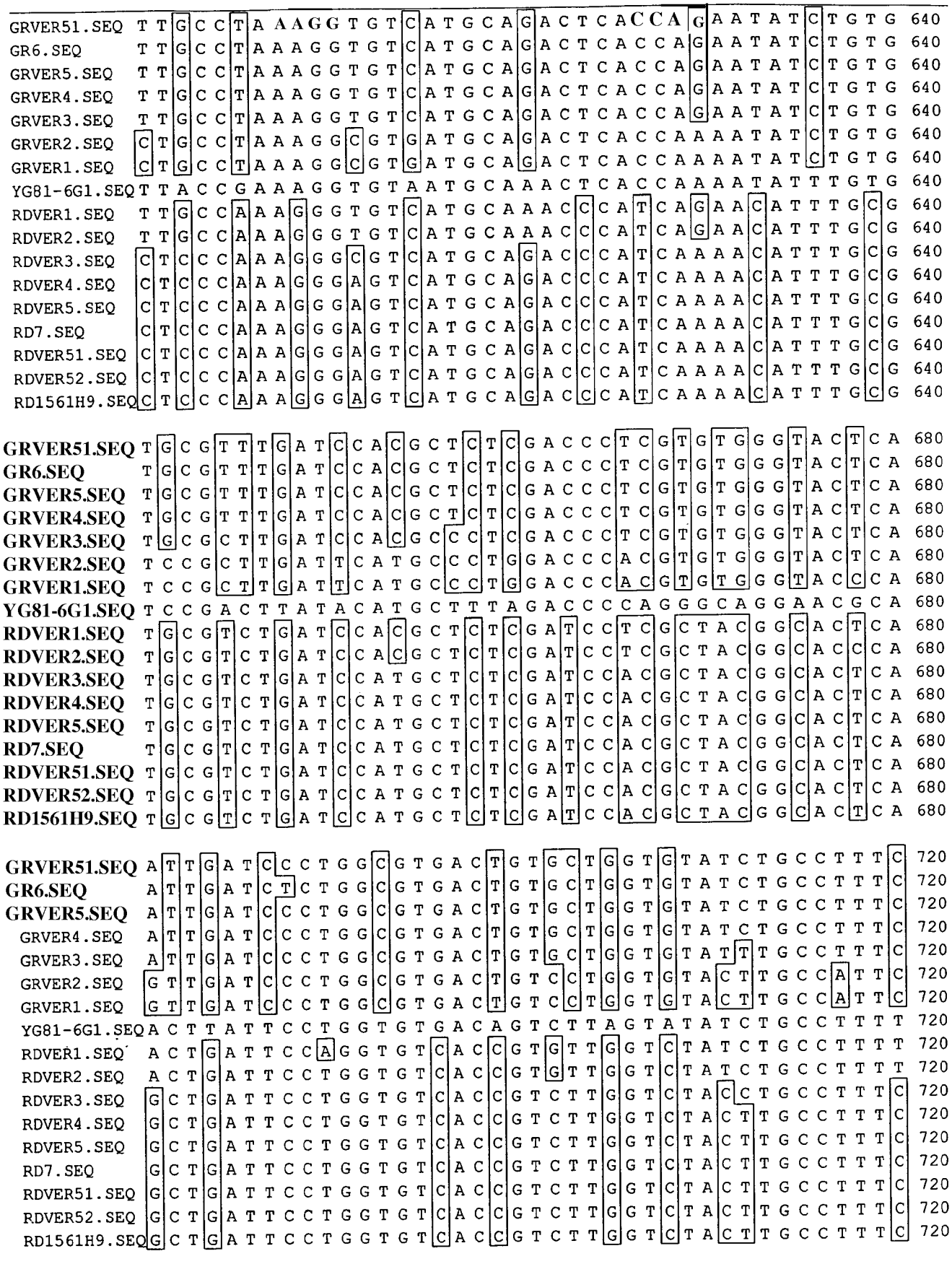
FIG. 2 (cont'd)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GRVER2.SEQ GTTGATCCCTGGCGTGACTGTCCTGGTGTACTTGCCATTTC 720
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RDVER2.SEQ ACTGATTCCTGGTGTCACCGTGTTGGTCTATCTGCCTTTTT 720
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RDVER5.SEQ GCTGATTCCTGGTGTCACCGTCTTGGTCTACTTGCCTTTTC 720
RD7.SEQ GCTGATTCCTGGTGTCACCGTCTTGGTCTACTTGCCTTTTC 720
RDVER51.SEQ GCTGATTCCTGGTGTCACCGTCTTGGTCTACTTGCCTTTTC 720
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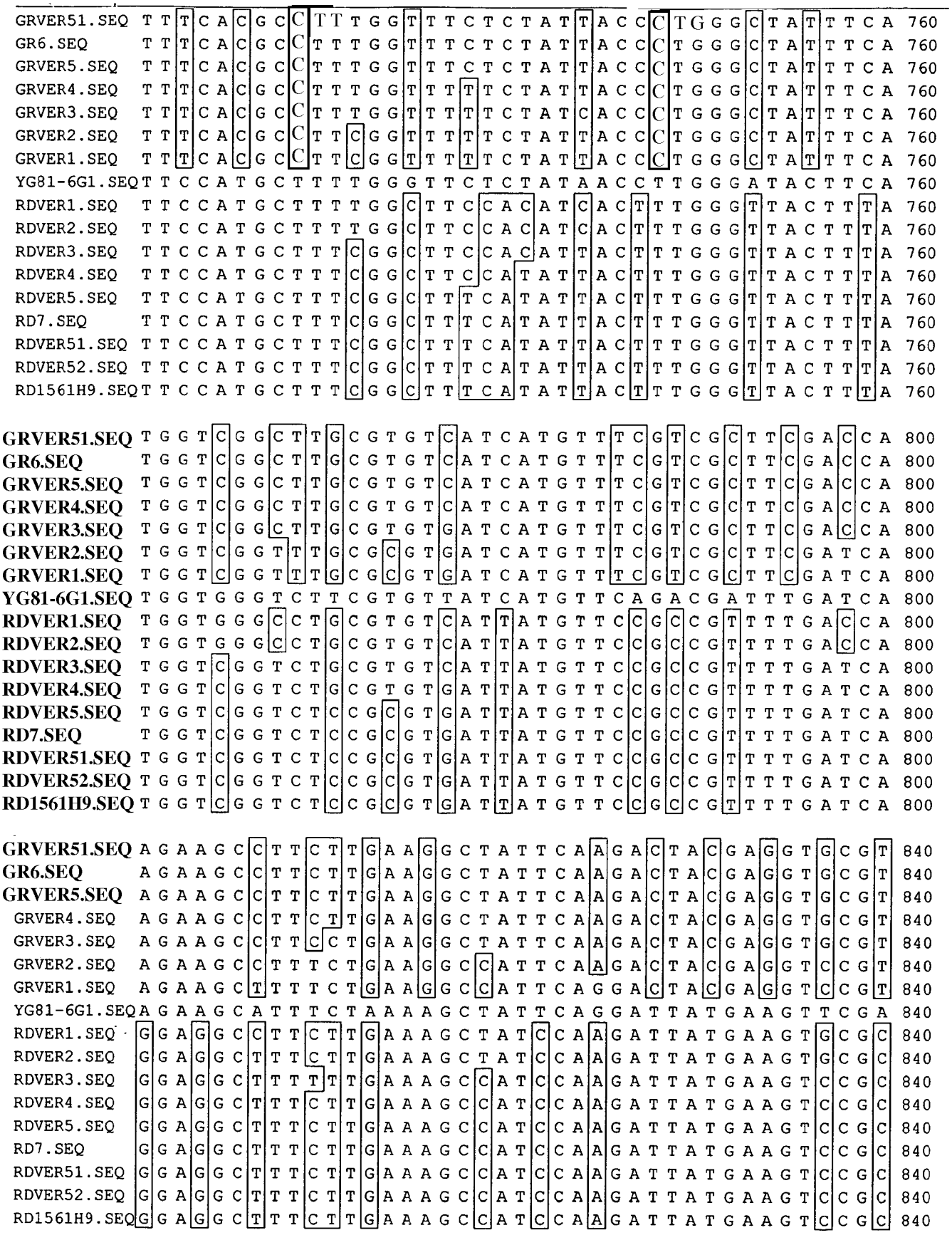
FIG. 2 (cont'd)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RDVER52.SEQ T T C C A T G C T T T C G G C T T T C A T A T T A C T T T G G G T T A C T T T A 760
RD1561H9.SEQ T T C C A T G C T T T C G G C T T T C A T A T T A C T T T G G G T T A C T T T A 760
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GRVER5.SEQ T G G T C G G C T T G C G T G T C A T C A T G T T T C G T C G C T T C G A C C A 800
GRVER4.SEQ T G G T C G G C T T G C G T G T C A T C A T G T T T C G T C G C T T C G A C C A 800
GRVER3.SEQ T G G T C G G C T T G C G T G T G A T C A T G T T T C G T C G C T T C G A C C A 800
GRVER2.SEQ T G G T C G G G T T T G C G C G T G A T C A T G T T T C G T C G C T T C G A T C A 800
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GRVER51.SEQ A G A A G C C T T C T T G A A G G C T A T T C A A G A C T A C G A G G T G C G T 840
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FIG. 2 (cont'd)

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GRVER4.SEQ  TCTGTCATCAATGTCCCTTCAGTCATTTTGTTCCTGAGCA 880
GRVER3.SEQ  TCTGTGATCAATGTCCCATCTGTCATTTTGTTCCTGAGCA 880
GRVER2.SEQ  AGCGTGATCAACGTCCCTTCTGTGATTTTGTTCCTGAGCA 880
GRVER1.SEQ  AGCGTGATCAACGTCCCTTCTGTGATTTTGTTCCTGAGCA 880
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RDVER2.SEQ  TCTGTCATTAATGTGCCAAGCGTCATCCTGTTTTTTGTCTA 880
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GR6.SEQ     TGAGCTGTGCTGTGGCGCTGCTCCTTGGCCAAAGAAGTG 960
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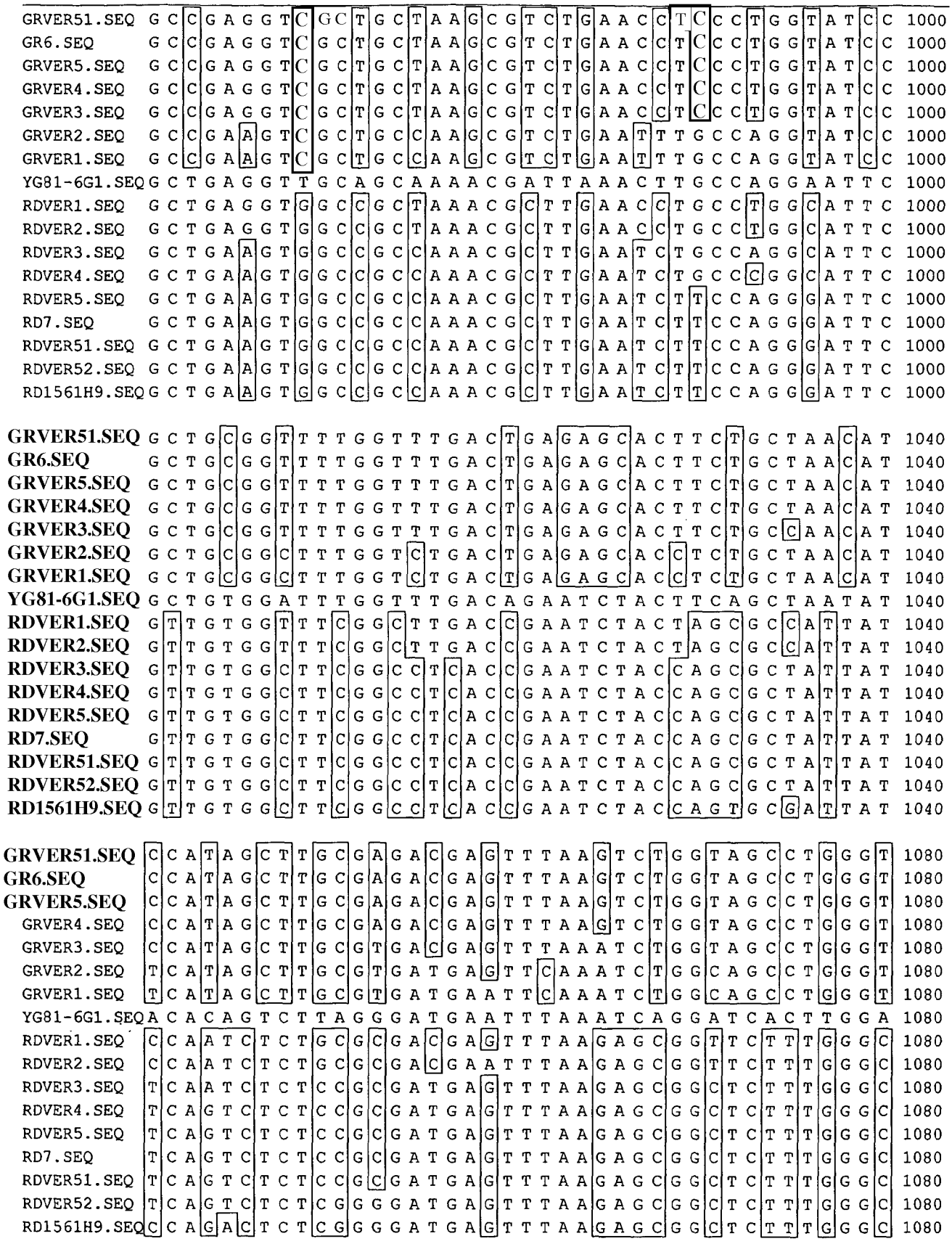
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RDVER51.SEQ GCTGAAGTGGCCGCCAAACGCTTGAATCTTCCAGGGATTC 1000
RDVER52.SEQ GCTGAAGTGGCCGCCAAACGCTTGAATCTTCCAGGGATTC 1000
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RDVER51.SEQ TCAGTCTCTCCGCGATGAGTTTAAGAGCGGCTCTTTGGGC 1080
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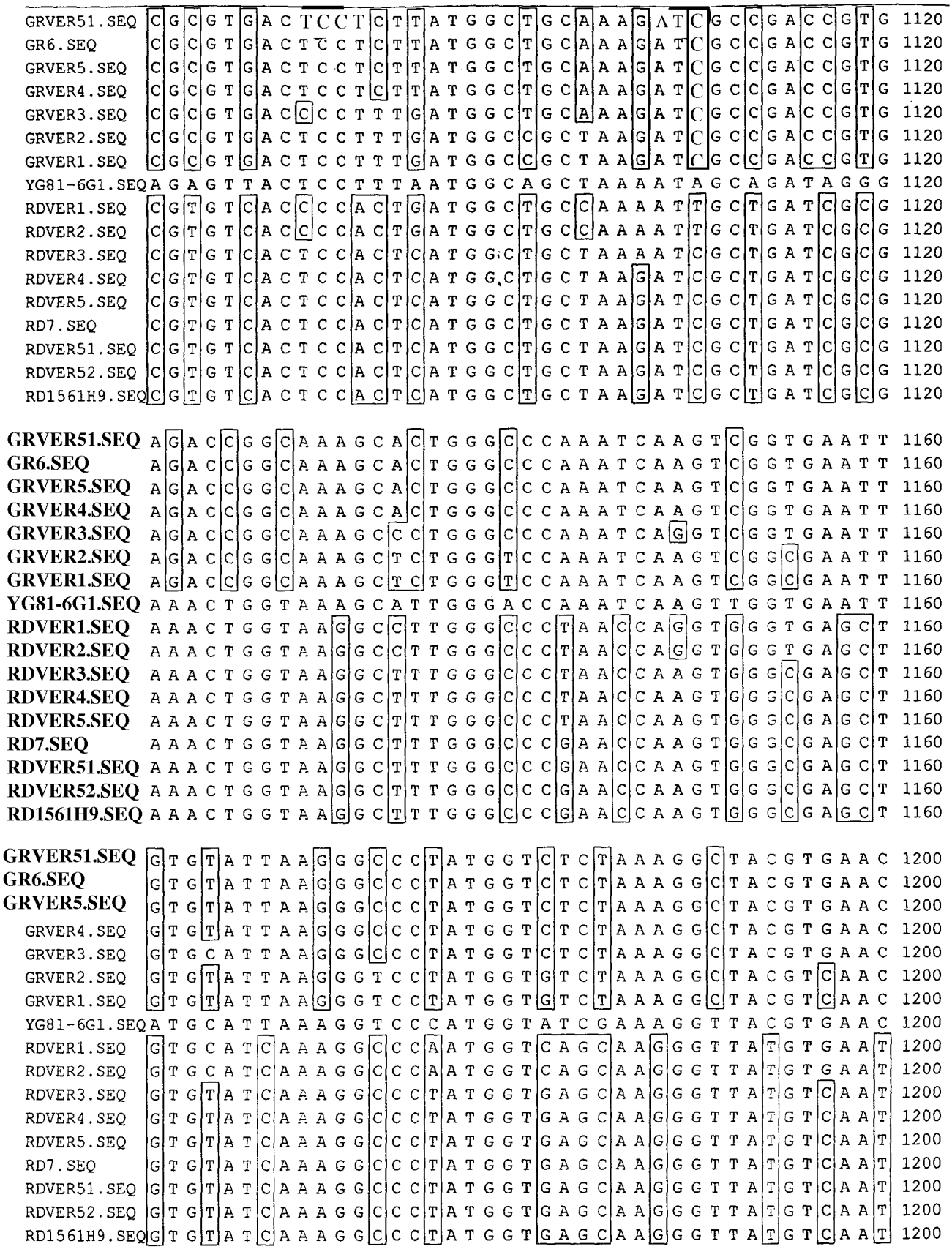
FIG. 2 (cont'd)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GRVER3.SEQ CGCGTGACCCTTTGATGGCTGCAAGATCGCCGACCGTG 1120
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FIG. 2 (cont'd)

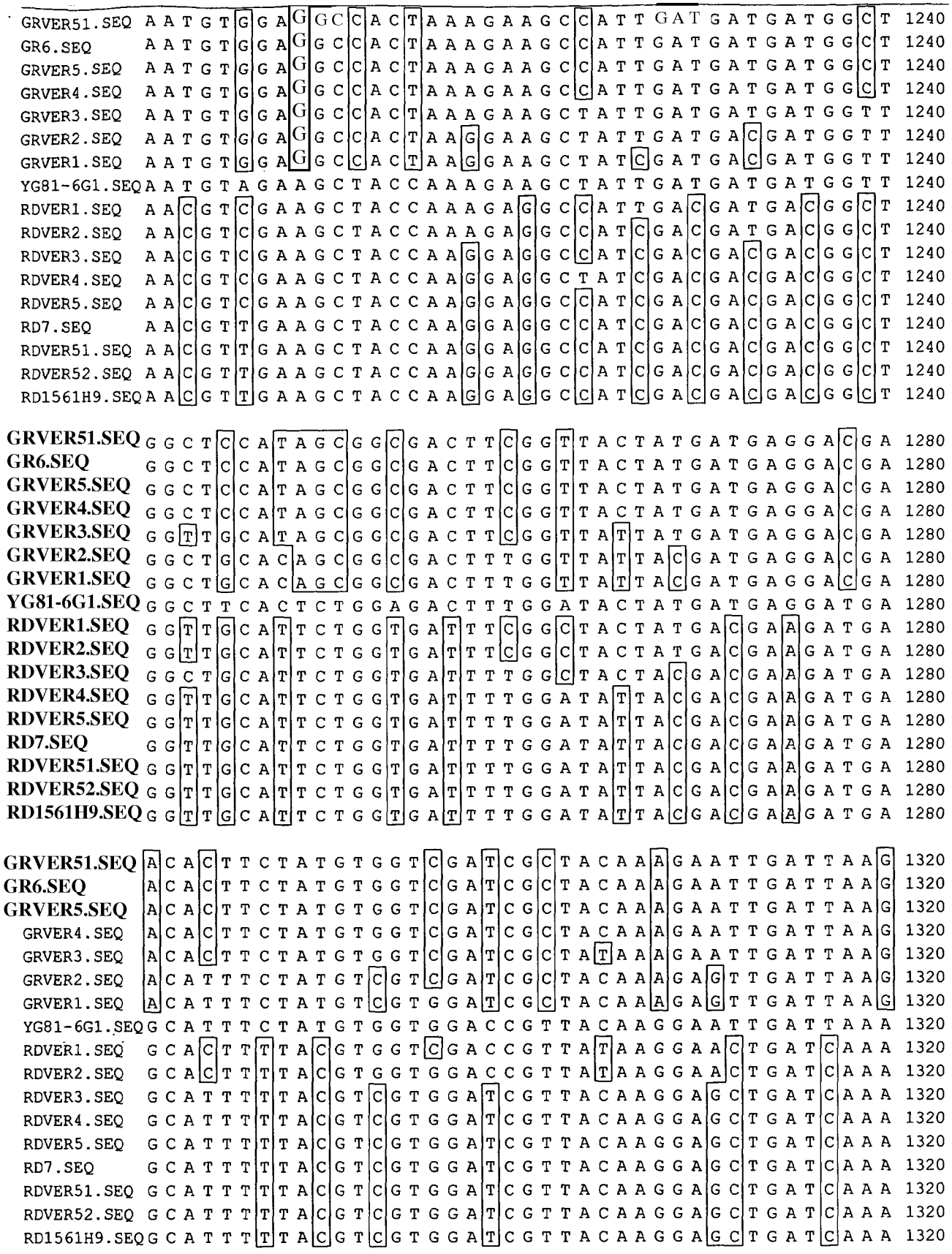

FIG. 2 (cont'd)

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GRVER1.SEQ   TATAAAGGCTCTCAGGTCGCCCCAGCTGAGCTGGAAGAGA 1360
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RDVER1.SEQ   TACAAGGGTAGCCAAGTGGCTCCTGCCGAATTGGAGGAAA 1360
RDVER2.SEQ   TACAAGGGTAGCCAAGTGGCTCCTGCCGAATTGGAGGAGA 1360
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RDVER5.SEQ   TACAAGGGTAGCCAGGTTGCTCCAGCTGAGTTGGAGGAGA 1360
RD7.SEQ      TACAAGGGTAGCCAGGTTGCTCCAGCTGAGTTGGAGGAGA 1360
RDVER51.SEQ  TACAAGGGTAGCCAGGTTGCTCCAGCTGAGTTGGAGGAGA 1360
RDVER52.SEQ  TACA'AGGGTAGCCAGGTTGCTCCAGCTGAGTTGGAGGAGA 1360
RD1561H9.SEQTACAAGGGTAGCCAGGTTGCTCCAGCTGAGTTGGAGGAGA 1360

GRVER51.SEQ  TTTTGCTGAAGAACCCTTGTATCCGCGACGTGGCCGTCGT 1400
GR6.SEQ      TTTTGCTGAAGAACCCTTGTATCCGCGACGTGGCCGTCGT 1400
GRVER5.SEQ   TTTTGCTGAAGAACCCTTGTATCCGCGACGTGGCCGTCGT 1400
GRVER4.SEQ   TTTTGCTGAAGAACCCTTGTATCCGCGACGTGGCCGTCGT 1400
GRVER3.SEQ   TTTTGCTGAAGAACCCTTGTATTCGCGACGTGGCCGTCGT 1400
GRVER2.SEQ   TCTTGCTGAAGAACCCTTGCATTCGTGACGTGGCCGTCGT 1400
GRVER1.SEQ   TCTTGCTGAAGAACCCTTGCATTCGTGACGTGGCCGTCGT 1400
YG81-6G1.SEQ TTTTATTGAAAAAATCCATGTATCAGAGATGTTGCTGTGGT 1400
RDVER1.SEQ   TTCTGTTGAAAAAATCCATGTATCCGCGATGTCGCTGTGGT 1400
RDVER2.SEQ   TTCTGTTGAAAAAATCCATGTATCCGCGATGTCGCTGTGGT 1400
RDVER3.SEQ   TTCTGTTGAAAAAATCCATGCATCCGTGATGTCGCTGTGGT 1400
RDVER4.SEQ   TTCTGTTGAAAAAATCCATGCATTCGCGATGTCGCTGTGGT 1400
RDVER5.SEQ   TTCTGTTGAAAAAATCCATGCATTCGCGATGTCGCTGTGGT 1400
RD7.SEQ      TTCTGTTGAAAAAATCCATGCATTCGCGATGTCGCTGTGGT 1400
RDVER51.SEQ  TTCTGTTGAAAAAATCCATGCATTCGCGATGTCGCTGTGGT 1400
RDVER52.SEQ  TTCTGTTGAAAAAATCCATGCATTCGCGATGTCGCTGTGGT 1400
RD1561H9.SEQTTCTGTTGAAAAAATCCATGCATTCGCGATGTCGCTGTGGT 1400

GRVER51.SEQ  GGGTATCCCAGACTTGGAAGCTGGCGAGTTGCCTAGCGCC 1440
GR6.SEQ      GGGTATCCCAGACTTGGAAGCTGGCGAGTTGCCTAGCGCC 1440
GRVER5.SEQ   GGGTATCCCAGACTTGGAAGCTGGCGAGTTGCCTAGCGCC 1440
GRVER4.SEQ   GGGTATCCCAGACTTGGAAGCTGGTGAGTTGCCTAGCGCC 1440
GRVER3.SEQ   GGGTATCCCAGACTTGGAAGCTGGCGAGTTGCCTAGCGCC 1440
GRVER2.SEQ   GGGTATCCCAGATTTGGAAGCTGGCGAGCTGCCTAGCGCC 1440
GRVER1.SEQ   GGGTATCCCAGATTTGGAAGCTGGCGAGCTGCCTAGCGCC 1440
YG81-6G1.SEQTGGTATTCCTGATCTAGAAGCTGGAGAACTGCCATCTGCG 1440
RDVER1.SEQ   CGGCATTCCTGACCTGGAGGCCGGTGAATTGCCATCTGCT 1440
RDVER2.SEQ   CGGCATTCCTGACCTGGAGGCCGGTGAATTGCCATCTGCT 1440
RDVER3.SEQ   CGGCATTCCTGATCTGGAGGCCGGTGAACTGCCTTCTGCT 1440
RDVER4.SEQ   CGGCATTCCTGATCTGGAGGCCGGCGAACTGCCTTCTGCT 1440
RDVER5.SEQ   CGGCATTCCTGATCTGGAGGCCGGCGAACTGCCTTCTGCT 1440
RD7.SEQ      CGGCATTCCTGATCTGGAGGCCGGCGAACTGCCTTCTGCT 1440
RDVER51.SEQ  CGGCATTCCTGATCTGGAGGCCGGCGAACTGCCTTCTGCT 1440
RDVER52.SEQ  CGGCATTCCTGATCTGGAGGCCGGCGAACTGCCTTCTGCT 1440
RD1561H9.SEQCGGCATTCCTGATCTGGAGGCCGGCGAACTGCCTTCTGCT 1440
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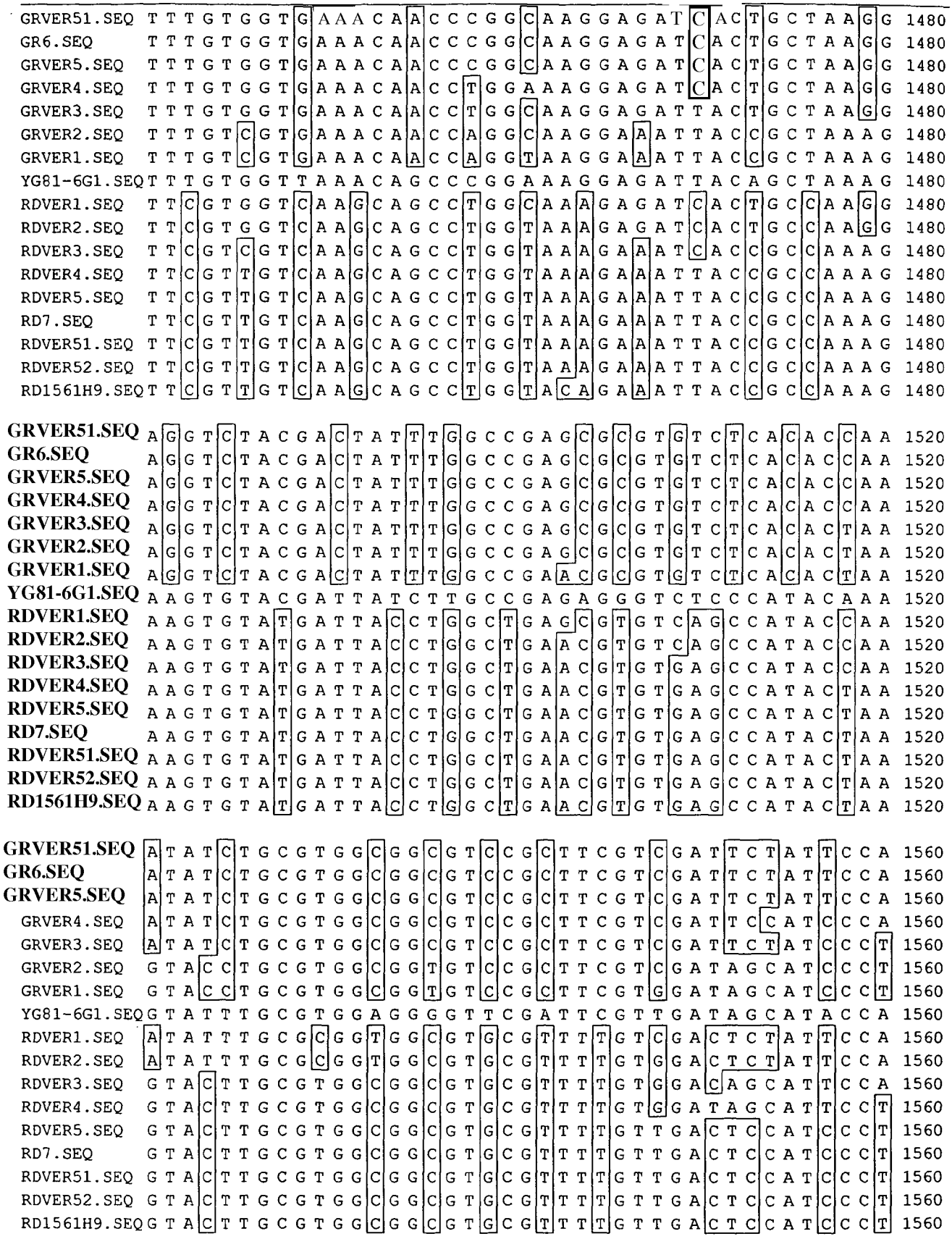
FIG. 2 (cont'd)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GR6.SEQ TTTGTGGTGAAACAACCCGGCAAGGAGATCACTGCTAAGG 1480
GRVER5.SEQ TTTGTGGTGAAACAACCCGGCAAGGAGATCACTGCTAAGG 1480
GRVER4.SEQ TTTGTGGTGAAACAACCTGGAAAGGAGATCACTGCTAAGG 1480
GRVER3.SEQ TTTGTGGTGAAACAACCTGGCAAGGAGATTACTGCTAAGG 1480
GRVER2.SEQ TTTGTCGTGAAACAACCAGGCAAGGAAATTACCGCTAAAAG 1480
GRVER1.SEQ TTTGTCGTGAAACAACCAGGTAAGGAAATTACCGCTAAAAG 1480
YG81-6G1.SEQ TTTGTGGTTAAAACAGCCCGGAAAGGAGATTACAGCTAAAAG 1480
RDVER1.SEQ TTCGTGGTCAAGCAGCCTGGCAAAGAGATCACTGCCAAGG 1480
RDVER2.SEQ TTCGTGGTCAAGCAGCCTGGTAAAGAGATCACTGCCAAGG 1480
RDVER3.SEQ TTCGTCGTCAAGCAGCCTGGTAAAGAAATCACCGCCAAAG 1480
RDVER4.SEQ TTCGTTGTCAAGCAGCCTGGTAAAGAAATTACCGCCAAAG 1480
RDVER5.SEQ TTCGTTGTCAAGCAGCCTGGTAAAGAAATTACCGCCAAAG 1480
RD7.SEQ TTCGTTGTCAAGCAGCCTGGTAAAGAAATTACCGCCAAAG 1480
RDVER51.SEQ TTCGTTGTCAAGCAGCCTGGTAAAGAAATTACCGCCAAAG 1480
RDVER52.SEQ TTCGTTGTCAAGCAGCCTGGTAAAGAAATTACCGCCAAAG 1480
RD1561H9.SEQ TTCGTTGTCAAGCAGCCTGGTACAGAATTACCGCCAAAG 1480
GRVER51.SEQ AGGTCTACGACTATTTGGCCGAGCGCGTGTCTCACACCAA 1520
GR6.SEQ AGGTCTACGACTATTTGGCCGAGCGCGTGTCTCACACCAA 1520
GRVER5.SEQ AGGTCTACGACTATTTGGCCGAGCGCGTGTCTCACACCAA 1520
GRVER4.SEQ AGGTCTACGACTATTTGGCCGAGCGCGTGTCTCACACCAA 1520
GRVER3.SEQ AGGTCTACGACTATTTGGCCGAGCGCGTGTCTCACACTAA 1520
GRVER2.SEQ AGGTCTACGACTATTTGGCCGAGCGCGTGTCTCACACTAA 1520
GRVER1.SEQ AGGTCTACGACTATTTGGCCGAACGCGTGTCTCACACTAA 1520
YG81-6G1.SEQ AAGTGTACGATTATCTTGCCGAGAGGGTCTCCCATACAAA 1520
RDVER1.SEQ AAGTGTATGATTACCTGGCTGAGCGTGTCAGCCATACCAA 1520
RDVER2.SEQ AAGTGTATGATTACCTGGCTGAACGTGTCAGCCATACCAA 1520
RDVER3.SEQ AAGTGTATGATTACCTGGCTGAACGTGTGAGCCATACCAA 1520
RDVER4.SEQ AAGTGTATGATTACCTGGCTGAACGTGTGAGCCATACTAA 1520
RDVER5.SEQ AAGTGTATGATTACCTGGCTGAACGTGTGAGCCATACTAA 1520
RD7.SEQ AAGTGTATGATTACCTGGCTGAACGTGTGAGCCATACTAA 1520
RDVER51.SEQ AAGTGTATGATTACCTGGCTGAACGTGTGAGCCATACTAA 1520
RDVER52.SEQ AAGTGTATGATTACCTGGCTGAACGTGTGAGCCATACTAA 1520
RD1561H9.SEQ AAGTGTATGATTACCTGGCTGAACGTGTGAGCCATACTAA 1520
GRVER51.SEQ ATATCTGCGTGGCGGCGTCCGCTTCGTCGATTCTATTCCA 1560
GR6.SEQ ATATCTGCGTGGCGGCGTCCGCTTCGTCGATTCTATTCCA 1560
GRVER5.SEQ ATATCTGCGTGGCGGCGTCCGCTTCGTCGATTCTATTCCA 1560
GRVER4.SEQ ATATCTGCGTGGCGGCGTCCGCTTCGTCGATTCCATCCCA 1560
GRVER3.SEQ ATATCTGCGTGGCGGCGTCCGCTTCGTCGATTCTATCCCT 1560
GRVER2.SEQ GTACCTGCGTGGCGGGTGTCCGCTTCGTCGATAGCATCCCT 1560
GRVER1.SEQ GTACCTGCGTGGCGGGTGTCCGCTTCGTGGATAGCATCCCT 1560
YG81-6G1.SEQ GTATTTGCGTGGAGGGGTTCGATTCGTTGATAGCATACCA 1560
RDVER1.SEQ ATATTTGCGCGGTGGCGTGCGTTTTGTGTCGACTCTATTCCA 1560
RDVER2.SEQ ATATTTGCGCGGTGGCGTGCGTTTTGTGGACTCTATTCCA 1560
RDVER3.SEQ GTACTTGCGTGGCGGCGTGCGTTTTGTGGACAGCATTCCA 1560
RDVER4.SEQ GTACTTGCGTGGCGGCGTGCGTTTTGTGGATAGCATTCCT 1560
RDVER5.SEQ GTACTTGCGTGGCGGCGTGCGTTTTGTTGACTCCATCCCT 1560
RD7.SEQ GTACTTGCGTGGCGGCGTGCGTTTTGTTGACTCCATCCCT 1560
RDVER51.SEQ GTACTTGCGTGGCGGCGTGCGTTTTGTTGACTCCATCCCT 1560
RDVER52.SEQ GTACTTGCGTGGCGGCGTGCGTTTTGTTGACTCCATCCCT 1560
RD1561H9.SEQ GTACTTGCGTGGCGGCGTGCGTTTTGTTGACTCCATCCCT 1560

FIG. 2 (cont'd)

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GRVER51.SEQ CGCAACGTTACCGGTAAGATCACTCGTAAAGAGTTGCTGA 1600
GR6.SEQ     CGCAACGTTACCGGTAAGATCACTCGTAAAGAGTTGCTGA 1600
GRVER5.SEQ  CGCAACGTTACCGGTAAGATCACTCGTAAAGAGTTGCTGA 1600
GRVER4.SEQ  CGCAACGTGACCGGTAAGATCACTCGTAAAGAATTGCTGA 1600
GRVER3.SEQ  CGCAACGTCACCGGCAAGATCACTCGTAAAGAGTTGCTGA 1600
GRVER2.SEQ  CGCAATGTCACCGGCAAAATTACTCGTAAGGAGTTGCTGA 1600
GRVER1.SEQ  CGCAATGTCACCGGCAAAATTACTCGTAAGGAGTTGCTGA 1600
YG81-6G1.SEQAGGAATGTTACAGGTAAAATTACAAGAAAGGAACTTCTGA 1600
RDVER1.SEQ  CGTAACGTGACTGGTAAGATCACCCGCAAAGAACTGTTGA 1600
RDVER2.SEQ  CGTAACGTGACTGGTAAGATCACCCGCAAAGAACTGTTGA 1600
RDVER3.SEQ  CGTAATGTGACTGGTAAAATTACCCGCAAGGAACTGTTGA 1600
RDVER4.SEQ  CGCAATGTGACTGGCAAAATTACCCGCAAGGAGCTGTTGA 1600
RDVER5.SEQ  CGTAACGTAACAGGCAAAATTACCCGCAAGGAGCTGTTGA 1600
RD7.SEQ     CGTAACGTAACAGGCAAAATTACCCGCAAGGAGCTGTTGA 1600
RDVER51.SEQ CGTAACGTAACAGGCAAAATTACCCGCAAGGAGCTGTTGA 1600
RDVER52.SEQ CGTAACGTAACAGGCAAAATTACCCGCAAGGAGCTGTTGA 1600
RD1561H9.SEQCGTAACGTAACAGGCAAAATTACCCGCAAGGAGCTGTTGA 1600

GRVER51.SEQ AGCAACTCCTCGAAAAAGCTGGCGGC 1626
GR6.SEQ     AGCAACTCCTCGAAAAAGCTGGCGGC 1626
GRVER5.SEQ  AGCAACTCCTCGAAAAAGCTGGCGGC 1626
GRVER4.SEQ  AGCAACTCCTCGAAAAAGCTGGCGGC 1626
GRVER3.SEQ  AACAATTGCTCGAAAAAGCTGGCGGC 1626
GRVER2.SEQ  AACAGTTGCTGGAAAAGGCTGGTGGC 1626
GRVER1.SEQ  AACAGTTGCTGGAAAAGGCTGGTGGC 1626
YG81-6G1.SEQAGCAGTTGCTGGAGAAGGCGGGAGGT 1626
RDVER1.SEQ  AGCAACTGTTGGAGAAACGCCGGCGGT 1626
RDVER2.SEQ  AGCAACTGTTGGAGAAAGCCGGCGGT 1626
RDVER3.SEQ  AGCAATTGTTGGAGAAGGCCGGCGGT 1626
RDVER4.SEQ  AACAATTGTTGGAGAAGGCCGGCGGT 1626
RDVER5.SEQ  AACAATTGTTGGAGAAGGCCGGCGGT 1626
RD7.SEQ     AACAATTGTTGGAGAAGGCCGGCGGT 1626
RDVER51.SEQ AACAATTGTTGGAGAAGGCCGGCGGT 1626
RDVER52.SEQ AACAATTGTTGGAGAAGGCCGGCGGT 1626
RD1561H9.SEQAACAATTGTTGGTGAAGGCCGGCGGT 1626
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FIG. 2 (cont'd)

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GRVER51.SEQ M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A 118
GR6.SEQ     M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A 118
GRVER5.SEQ  M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A 118
GRVER4.SEQ  M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A 118
GRVER3.SEQ  M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A 118
GRVER2.SEQ  M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A 118
GRVER1.SEQ  M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A 118
YG81-6G1.SEQM M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A 118
RDVER1.SEQ  M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A 118
RDVER2.SEQ  M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A 118
RDVER3.SEQ  M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A 118
RDVER4.SEQ  M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A 118
RDVER5.SEQ  M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A 118
RD7.SEQ     M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S Y L P Q A 118
RDVER51.SEQ M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A 118
RDVER52.SEQ M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A 118
RD1561H9.SEQM I K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A 118

GRVER51.SEQ L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238
GR6.SEQ     L V D V V G D E N L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238
GRVER5.SEQ  L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238
GRVER4.SEQ  L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238
GRVER3.SEQ  L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238
GRVER2.SEQ  L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238
GRVER1.SEQ  L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238
YG81-6G1.SEQL V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238
RDVER1.SEQ  L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238
RDVER2.SEQ  L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238
RDVER3.SEQ  L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238
RDVER4.SEQ  L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238
RDVER5.SEQ  L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238
RD7.SEQ     L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238
RDVER51.SEQ L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238
RDVER52.SEQ L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238
RD1561H9.SEQL V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238

GRVER51.SEQ A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S 358
GR6.SEQ     A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S 358
GRVER5.SEQ  A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S 358
GRVER4.SEQ  A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S 358
GRVER3.SEQ  A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S 358
GRVER2.SEQ  A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S 358
GRVER1.SEQ  A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S 358
YG81-6G1.SEQA E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S 358
RDVER1.SEQ  A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S 358
RDVER2.SEQ  A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S 358
RDVER3.SEQ  A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S 358
RDVER4.SEQ  A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S 358
RDVER5.SEQ  A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S 358
RD7.SEQ     A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S 358
RDVER51.SEQ A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S 358
RDVER52.SEQ A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S 358
RD1561H9.SEQA E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S 358
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FIG. 3

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GRVER51.SEQ K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C 478
GR6.SEQ     K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C 478
GRVER5.SEQ  K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C 478
GRVER4.SEQ  K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C 478
GRVER3.SEQ  K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C 478
GRVER2.SEQ  K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C 478
GRVER1.SEQ  K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C 478
YG81-6G1.SEQK P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C 478
RDVER1.SEQ  K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C 478
RDVER2.SEQ  K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C 478
RDVER3.SEQ  K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C 478
RDVER4.SEQ  K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C 478
RDVER5.SEQ  K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C 478
RD7.SEQ     K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C 478
RDVER51.SEQ K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C 478
RDVER52.SEQ K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C 478
RD1561H9.SEQK P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C 478

GRVER51.SEQ E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G 598
GR6.SEQ     E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G 598
GRVER5.SEQ  E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G 598
GRVER4.SEQ  E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G 598
GRVER3.SEQ  E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G 598
GRVER2.SEQ  E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G 598
GRVER1.SEQ  E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G 598
YG81-6G1.SEQ E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G 598
RDVER1.SEQ  E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G 598
RDVER2.SEQ  E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G 598
RDVER3.SEQ  E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G 598
RDVER4.SEQ  E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G 598
RDVER5.SEQ  E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G 598
RD7.SEQ     E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G 598
RDVER51.SEQ E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G 598
RDVER52.SEQ E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G 598
RD1561H9.SEQE S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G 598

GRVER51.SEQ L P K G V M Q T H Q N I C V R L I H A L D P R V G T Q L I P G V T V L V Y L P F 718
GR6.SEQ     L P K G V M Q T H Q N I C V R L I H A L D P R V G T Q L I S G V T V L V Y L P F 718
GRVER5.SEQ  L P K G V M Q T H Q N I C V R L I H A L D P R V G T Q L I P G V T V L V Y L P F 718
GRVER4.SEQ  L P K G V M Q T H Q N I C V R L I H A L D P R V G T Q L I P G V T V L V Y L P F 718
GRVER3.SEQ  L P K G V M Q T H Q N I C V R L I H A L D P R V G T Q L I P G V T V L V Y L P F 718
GRVER2.SEQ  L P K G V M Q T H Q N I C V R L I H A L D P R V G T Q L I P G V T V L V Y L P F 718
GRVER1.SEQ  L P K G V M Q T H Q N I C V R L I H A L D P R V G T Q L I P G V T V L V Y L P F 718
YG81-6G1.SEQL P K G V M Q T H Q N I C V R L I H A L D P R A G T Q L I P G V T V L V Y L P F 718
RDVER1.SEQ  L P K G V M Q T H Q N I C V R L I H A L D P R Y G T Q L I P G V T V L V Y L P F 718
RDVER2.SEQ  L P K G V M Q T H Q N I C V R L I H A L D P R Y G T Q L I P G V T V L V Y L P F 718
RDVER3.SEQ  L P K G V M Q T H Q N I C V R L I H A L D P R Y G T Q L I P G V T V L V Y L P F 718
RDVER4.SEQ  L P K G V M Q T H Q N I C V R L I H A L D P R Y G T Q L I P G V T V L V Y L P F 718
RDVER5.SEQ  L P K G V M Q T H Q N I C V R L I H A L D P R Y G T Q L I P G V T V L V Y L P F 718
RD7.SEQ     L P K G V M Q T H Q N I C V R L I H A L D P R Y G T Q L I P G V T V L V Y L P F 718
RDVER51.SEQ L P K G V M Q T H Q N I C V R L I H A L D P R Y G T Q L I P G V T V L V Y L P F 718
RDVER52.SEQ L P K G V M Q T H Q N I C V R L I H A L D P R Y G T Q L I P G V T V L V Y L P F 718
RD1561H9.SEQL P K G V M Q T H Q N I C V R L I H A L D P R Y G T Q L I P G V T V L V Y L P F 718
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FIG. 3 (cont'd)

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GRVER51.SEQ  F H A F G F S I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R 838
GR6.SEQ      F H A F G F S I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R 838
GRVER5.SEQ   F H A F G F S I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R 838
GRVER4.SEQ   F H A F G F S I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R 838
GRVER3.SEQ   F H A F G F S I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R 838
GRVER2.SEQ   F H A F G F S I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R 838
GRVER1.SEQ   F H A F G F S I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R 838
YG81-6G1.SEQ F H A F G F S I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R 838
RDVER1.SEQ   F H A F G F H I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R 838
RDVER2.SEQ   F H A F G F H I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R 838
RDVER3.SEQ   F H A F G F H I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R 838
RDVER4.SEQ   F H A F G F H I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R 838
RDVER5.SEQ   F H A F G F H I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R 838
RD7.SEQ      F H A F G F H I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R 838
RDVER51.SEQ  F H A F G F H I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R 838
RDVER52.SEQ  F H A F G F H I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R 838
RD1561H9.SEQ F H A F G F H I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R 838

GRVER51.SEQ  S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V 958
GR6.SEQ      S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V 958
GRVER5.SEQ   S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V 958
GRVER4.SEQ   S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V 958
GRVER3.SEQ   S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V 958
GRVER2.SEQ   S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V 958
GRVER1.SEQ   S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V 958
YG81-6G1.SEQ S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V 958
RDVER1.SEQ   S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V 958
RDVER2.SEQ   S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V 958
RDVER3.SEQ   S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V 958
RDVER4.SEQ   S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V 958
RDVER5.SEQ   S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V 958
RD7.SEQ      S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V 958
RDVER51.SEQ  S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V 958
RDVER52.SEQ  S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V 958
RD1561H9.SEQ S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V 958

GRVER51.SEQ  A E V A A K R L N L P G I R C G F G L T E S T S A N I H S L R D E F K S G S L G 1078
GR6.SEQ      A E V A A K R L N L P G I R C G F G L T E S T S A N I H S L R D E F K S G S L G 1078
GRVER5.SEQ   A E V A A K R L N L P G I R C G F G L T E S T S A N I H S L R D E F K S G S L G 1078
GRVER4.SEQ   A E V A A K R L N L P G I R C G F G L T E S T S A N I H S L R D E F K S G S L G 1078
GRVER3.SEQ   A E V A A K R L N L P G I R C G F G L T E S T S A N I H S L R D E F K S G S L G 1078
GRVER2.SEQ   A E V A A K R L N L P G I R C G F G L T E S T S A N I H S L R D E F K S G S L G 1078
GRVER1.SEQ   A E V A A K R L N L P G I R C G F G L T E S T S A N I H S L R D E F K S G S L G 1078
YG81-6G1.SEQ A E V A A K R L N L P G I R C G F G L T E S T S A N I H S L R D E F K S G S L G 1078
RDVER1.SEQ   A E V A A K R L N L P G I R C G F G L T E S T S A I I Q S L R D E F K S G S L G 1078
RDVER2.SEQ   A E V A A K R L N L P G I R C G F G L T E S T S A I I Q S L R D E F K S G S L G 1078
RDVER3.SEQ   A E V A A K R L N L P G I R C G F G L T E S T S A I I Q S L R D E F K S G S L G 1078
RDVER4.SEQ   A E V A A K R L N L P G I R C G F G L T E S T S A I I Q S L R D E F K S G S L G 1078
RDVER5.SEQ   A E V A A K R L N L P G I R C G F G L T E S T S A I I Q S L R D E F K S G S L G 1078
RD7.SEQ      A E V A A K R L N L P G I R C G F G L T E S T S A I I Q S L R D E F K S G S L G 1078
RDVER51.SEQ  A E V A A K R L N L P G I R C G F G L T E S T S A I I Q S L R D E F K S G S L G 1078
RDVER52.SEQ  A E V A A K R L N L P G I R C G F G L T E S T S A I I Q S L G D E F K S G S L G 1078
RD1561H9.SEQ A E V A A K R L N L P G I R C G F G L T E S T S A I I Q T L G D E F K S G S L G 1078
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FIG. 3 (cont'd)

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GRVER51.SEQ R V T P L M A AKI A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N 1198
GR6.SEQ     R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N 1198
GRVER5.SEQ  R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N 1198
GRVER4.SEQ  R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N 1198
GRVER3.SEQ  R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N 1198
GRVER2.SEQ  R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N 1198
GRVER1.SEQ  R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N 1198
YG81-6G1.SEQR V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N 1198
RDVER1.SEQ  R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N 1198
RDVER2.SEQ  R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N 1198
RDVER3.SEQ  R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N 1198
RDVER4.SEQ  R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N 1198
RDVER5.SEQ  R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N 1198
RD7.SEQ     R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N 1198
RDVER51.SEQ R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N 1198
RDVER52.SEQ R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N 1198
RD1561H9.SEQR V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N 1198

GRVER51.SEQ N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
GR6.SEQ     N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
GRVER5.SEQ  N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
GRVER4.SEQ  N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
GRVER3.SEQ  N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
GRVER2.SEQ  N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
GRVER1.SEQ  N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
YG81-6G1.SEQN V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
RDVER1.SEQ  N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
RDVER2.SEQ  N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
RDVER3.SEQ  N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
RDVER4.SEQ  N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
RDVER5.SEQ  N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
RD7.SEQ     N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
RDVER51.SEQ N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
RDVER52.SEQ N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318
RD1561H9.SEQN V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K 1318

GRVER51.SEQ Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A 1438
GR6.SEQ     Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A 1438
GRVER5.SEQ  Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A 1438
GRVER4.SEQ  Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A 1438
GRVER3.SEQ  Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A 1438
GRVER2.SEQ  Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A 1438
GRVER1.SEQ  Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A 1438
YG81-6G1.SEQY K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A 1438
RDVER1.SEQ  Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A 1438
RDVER2.SEQ  Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A 1438
RDVER3.SEQ  Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A 1438
RDVER4.SEQ  Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A 1438
RDVER5.SEQ  Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A 1438
RD7.SEQ     Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A 1438
RDVER51.SEQ Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A 1438
RDVER52.SEQ Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A 1438
RD1561H9.SEQY K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A 1438
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FIG. 3 (cont'd)

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GRVER51.SEQ  F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
GR6.SEQ      F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
GRVER5.SEQ   F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
GRVER4.SEQ   F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
GRVER3.SEQ   F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
GRVER2.SEQ   F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
GRVER1.SEQ   F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
YG81-6G1.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
RDVER1.SEQ   F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
RDVER2.SEQ   F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
RDVER3.SEQ   F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
RDVER4.SEQ   F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
RDVER5.SEQ   F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
RD7.SEQ      F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
RDVER51.SEQ  F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
RDVER52.SEQ  F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
RD1561H9.SEQ F V V K Q P G [T] E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558

GRVER51.SEQ  R N V T G K I T R K E L L K Q L L E K A G G 1624
GR6.SEQ      R N V T G K I T R K E L L K Q L L E K A G G 1624
GRVER5.SEQ   R N V T G K I T R K E L L K Q L L E K A G G 1624
GRVER4.SEQ   R N V T G K I T R K E L L K Q L L E K A G G 1624
GRVER3.SEQ   R N V T G K I T R K E L L K Q L L E K A G G 1624
GRVER2.SEQ   R N V T G K I T R K E L L K Q L L E K A G G 1624
GRVER1.SEQ   R N V T G K I T R K E L L K Q L L E K A G G 1624
YG81-6G1.SEQ R N V T G K I T R K E L L K Q L L E K A G G 1624
RDVER1.SEQ   R N V T G K I T R K E L L K Q L L E K A G G 1624
RDVER2.SEQ   R N V T G K I T R K E L L K Q L L E K A G G 1624
RDVER3.SEQ   R N V T G K I T R K E L L K Q L L E K A G G 1624
RDVER4.SEQ   R N V T G K I T R K E L L K Q L L E K A G G 1624
RDVER5.SEQ   R N V T G K I T R K E L L K Q L L E K A G G 1624
RD7.SEQ      R N V T G K I T R K E L L K Q L L E K A G G 1624
RDVER51.SEQ  R N V T G K I T R K E L L K Q L L E K A G G 1624
RDVER52.SEQ  R N V T G K I T R K E L L K Q L L E K A G G 1624
RD1561H9.SEQ R N V T G K I T R K E L L K Q L L [V] K A G G 1624
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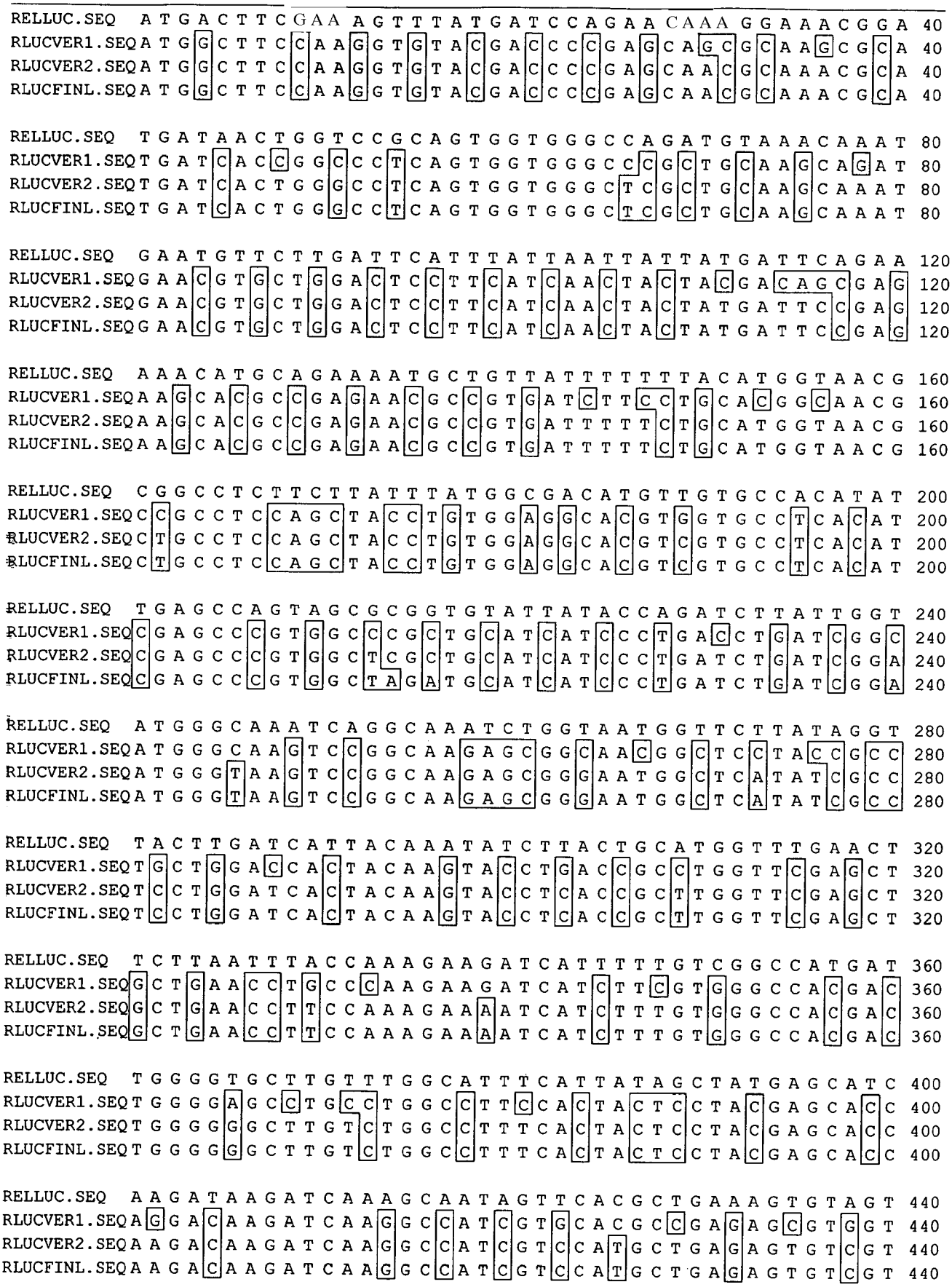
FIG. 3 (cont'd)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RLUCVER1.SEQ ATGGCTTCCAAGGTGTACGACCCCGAGCAGCGCAAGCGCA 40
RLUCVER2.SEQ ATGGCTTCCAAGGTGTACGACCCCGAGCAAACGCAAACGCA 40
RLUCFINL.SEQ ATGGCTTCCAAGGTGTACGACCCCGAGCAACGCAAACGCA 40
RELLUC.SEQ TGATAACTGGTCCGCAGTGGTGGGCCAGATGTAAACAAAT 80
RLUCVER1.SEQ TGATCACCGGCCCTCAGTGGTGGGCCCGCTGCAAGCAGAT 80
RLUCVER2.SEQ TGATCACTGGGCCTCAGTGGTGGGCTCGCTGCAAGCAAAT 80
RLUCFINL.SEQ TGATCACTGGGCCTCAGTGGTGGGCTCGCTGCAAGCAAAT 80
RELLUC.SEQ GAATGTTCTTGATTCATTTATTAATTATTATGATTCAGAA 120
RLUCVER1.SEQ GAACGTGCTGGACTCCTTCATCAACTACTACGACAGCGAG 120
RLUCVER2.SEQ GAACGTGCTGGACTCCTTCATCAACTACTATGATTCCGAG 120
RLUCFINL.SEQ GAACGTGCTGGACTCCTTCATCAACTACTATGATTCCGAG 120
RELLUC.SEQ AAACATGCAGAAAATGCTGTTATTTTTTTACATGGTAACG 160
RLUCVER1.SEQ AAGCACGCCGAGAACGCCGTGATCTTCCTGCACGGCAACG 160
RLUCVER2.SEQ AAGCACGCCGAGAACGCCGTGATTTTTCTGCATGGTAACG 160
RLUCFINL.SEQ AAGCACGCCGAGAACGCCGTGATTTTTCTGCATGGTAACG 160
RELLUC.SEQ CGGCCTCTTCTTATTTATGGCGACATGTTGTGCCACATAT 200
RLUCVER1.SEQ CCGCCTCCAGCTACCTGTGGAGGCACGTGGTGCCTCACCAT 200
RLUCVER2.SEQ CTGCCTCCAGCTACCTGTGGAGGCACGTCGTGCCTCACCAT 200
RLUCFINL.SEQ CTGCCTCCAGCTACCTGTGGAGGCACGTCGTGCCTCACCAT 200
RELLUC.SEQ TGAGCCAGTAGCGCGGTGTATTATACCAGATCTTATTGGT 240
RLUCVER1.SEQ CGAGCCCGTGGCCCGCTGCATCATCCCTGACCTGGATCGGC 240
RLUCVER2.SEQ CGAGCCCGTGGCCTCGCTGCATCATCCCTGATCTGGATCGGA 240
RLUCFINL.SEQ CGAGCCCGTGGCCTAGATGCATCATCCCTGATCTGGATCGGA 240
RELLUC.SEQ ATGGGCAAAATCAGGCAAATCTGGTAATGGTTCTTATAGGT 280
RLUCVER1.SEQ ATGGGCAAGTCCGGCAAGAGCGGCAACGGCTCCTACCGCC 280
RLUCVER2.SEQ ATGGGTAAGTCCGGCAAGAGCGGGAATGGCTCATATCGCC 280
RLUCFINL.SEQ ATGGGTAAGTCCGGCAAGAGCGGGAATGGCTCATATCGCC 280
RELLUC.SEQ TACTTGATCATTACAAATATCTTACTGCATGGTTTGAACT 320
RLUCVER1.SEQ TGCTGGACCACTACAAGTACCTGACCGCCTGGTTCGAGCT 320
RLUCVER2.SEQ TCCTGGATCACTACAAGTACCTCACCGCTTGGTTCGAGCT 320
RLUCFINL.SEQ TCCTGGATCACTACAAGTACCTCACCGCTTGGTTCGAGCT 320
RELLUC.SEQ TCTTAATTTACCAAAGAAGATCATTTTTGTCGGCCATGAT 360
RLUCVER1.SEQ GCTGAACCTGCCCAAGAAGATCATCTTCGTGGGCCACGAC 360
RLUCVER2.SEQ GCTGAACCTTCCAAAGAAAATCATCTTTGTGGGCCACGAC 360
RLUCFINL.SEQ GCTGAACCTTCCAAAGAAAATCATCTTTGTGGGCCACGAC 360
RELLUC.SEQ TGGGGTGCTTGTTTGGCATTTCATTATAGCTATGAGCATC 400
RLUCVER1.SEQ TGGGGAGCCTGCCTGGCCTTCCACTACTCCTACGAGCACC 400
RLUCVER2.SEQ TGGGGGGCTTGTCTGGCCTTTCACTACTCCTACGAGCACC 400
RLUCFINL.SEQ TGGGGGGCTTGTCTGGCCTTTCACTACTCCTACGAGCACC 400
RELLUC.SEQ AAGATAAGATCAAAGCAATAGTTCACGCTGAAAGTGTAGT 440
RLUCVER1.SEQ AGGACAAGATCAAGGCCCATCGTGCACGCCGAGAGCGTGGT 440
RLUCVER2.SEQ AAGACAAGATCAAGGCCCATCGTCCATGCTGAGAGTGTCGT 440
RLUCFINL.SEQ AAGACAAGATCAAGGCCCATCGTCCATGCTGAGAGTGTCGT 440

FIG. 7

```
RELLUC.SEQ   AGATGTGATTGAATCATGGGATGAATG GCCTGATATTGAA 480
RLUCVER1.SEQGGACGTGATCGAGTCCTGGGACGAGTGGCCTGACATCGAG 480
RLUCVER2.SEQGGACGTGATCGAGTCCTGGGACGAGTGGCCTGACATCGAG 480
RLUCFINL.SEQGGACGTGATCGAGTCCTGGGACGAGTGGCCTGACATCGAG 480

RELLUC.SEQ   GAAGATATTGCGTTGATCAAATCTGAAGAAGGAGAAAAAA 520
RLUCVER1.SEQGAGGACATCGCCCTGATCAAGAGCGAGGAGGCGAGAAGA 520
RLUCVER2.SEQGAGGATATCGCCCTGATCAAGAGCGAAGAGGGCGAGAAAA 520
RLUCFINL.SEQGAGGATATCGCCCTGATCAAGAGCGAAGAGGGCGAGAAAA 520

RELLUC.SEQ   TGGTTTTGGAGAATAACTTCTTCGTGGAAACCATGTTGCC 560
RLUCVER1.SEQTGGTGCTGGAGAACAACTTCTTCGTGGAGACCATGCTGCC 560
RLUCVER2.SEQTGGTGCTTGAGAATAACTTCTTCGTCGAGACCATGCTCCC 560
RLUCFINL.SEQTGGTGCTTGAGAATAACTTCTTCGTCGAGACCATGCTCCC 560

RELLUC.SEQ   ATCAAAAATCATGAGAAAGTTAGAACCAGAAGAATTTGCA 600
RLUCVER1.SEQCAGCAAGATCATGCGCAAGCTGGAGCCTGAGGAGTTCGCC 600
RLUCVER2.SEQAAGCAAGATCATGCGGAAACTGGAGCCTGAGGAGTTCGCT 600
RLUCFINL.SEQAAGCAAGATCATGCGGAAACTGGAGCCTGAGGAGTTCGCT 600

RELLUC.SEQ   GCATATCTTGAACCATTCAAAGAGAAAGGTGAAGTTCGTC 640
RLUCVER1.SEQGCCTACCTGGAGCCCTTCAAGGAGAAGGGCGAGGTGCGCC 640
RLUCVER2.SEQGCCTACCTGGAGCCCTTCAAGGAGAAGGGCGAGGTTAGAC 640
RLUCFINL.SEQGCCTACCTGGAGCCATTCAAGGAGAAGGGCGAGGTTAGAC 640

RELLUC.SEQ   GTCCAACATTATCATGGCCTCGTGAAATCCCGTTAGTAAA 680
RLUCVER1.SEQGCCCTACCCTGTCCTGGCCCCGCGAGATCCCTCTGGTGAA 680
RLUCVER2.SEQGGCCTACCCTCTCCTGGCCTCGCGAGATCCCTCTCGTTAA 680
RLUCFINL.SEQGGCCTACCCTCTCCTGGCCTCGCGAGATCCCTCTCGTTAA 680

RELLUC.SEQ   AGGTGGTAAACCTGACGTTGTACAAATTGTTAGGAATTAT 720
RLUCVER1.SEQGGGCGGCAAGCCCGACGTGGTGCAGATCGTGCGCAACTAC 720
RLUCVER2.SEQGGGAGGCAAGCCCGACGTCGTCCAGATTGTCCGCAACTAC 720
RLUCFINL.SEQGGGAGGCAAGCCCGACGTCGTCCAGATTGTCCGCAACTAC 720

RELLUC.SEQ   AATGCTTATCTACGTGCAAGTGATGATTTACCAAAAATGT 760
RLUCVER1.SEQAACGCCTACCTGCGCGCCAGCGACGACCTGCCTAAGATGT 760
RLUCVER2.SEQAACGCCTACCTTCGGGCCAGCGACGATCTGCCTAAGATGT 760
RLUCFINL.SEQAACGCCTACCTTCGGGCCAGCGACGATCTGCCTAAGATGT 760

RELLUC.SEQ   TTATTGAATCGGATCCAGGATTCTTTTCCAATGCTATTGT 800
RLUCVER1.SEQTCATCGAGTCCGACCCTGGCTTCTTCTCCAACGCCATCGT 800
RLUCVER2.SEQTCATCGAGTCCGACCCTGGGTTCTTTTCCAACGCTATTGT 800
RLUCFINL.SEQTCATCGAGTCCGACCCTGGGTTCTTTTCCAACGCTATTGT 800

RELLUC.SEQ   TGAAGGCGCCAAGAAGTTTCCTAATACTGAATTTGTCAAA 840
RLUCVER1.SEQCGAGGGAGCCAAGAAGTTCCCCAACACCGAGTTCGTGAAG 840
RLUCVER2.SEQCGAGGGAGCTAAGAAGTTCCCTAACACCGAGTTCGTGAAG 840
RLUCFINL.SEQCGAGGGAGCTAAGAAGTTCCCTAACACCGAGTTCGTGAAG 840

RELLUC.SEQ   GTAAAAGGTCTTCATTTTTCGCAAGAAGATGCACCTGATG 880
RLUCVER1.SEQGTGAAGGGCCTGCACTTCTCCCAGGAGGACGCCCCTGACG 880
RLUCVER2.SEQGTGAAGGGCCTCCACTTCAGCCAGGAGGACGCTCCAGATG 880
RLUCFINL.SEQGTGAAGGGCCTCCACTTCAGCCAGGAGGACGCTCCAGATG 880
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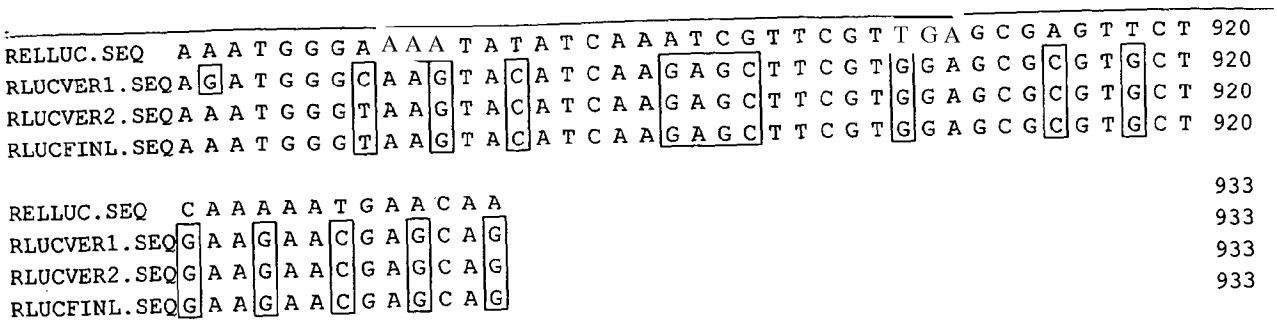
FIG. 7 (cont'd)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RLUCVER1.SEQ A G A T G G G C A A G T A C A T C A A G A G C T T C G T G G A G C G C G T G C T 920
RLUCVER2.SEQ A A A T G G G T A A G T A C A T C A A G A G C T T C G T G G A G C G C G T G C T 920
RLUCFINL.SEQ A A A T G G G T A A G T A C A T C A A G A G C T T C G T G G A G C G C G T G C T 920
933
RELLUC.SEQ C A A A A A T G A A C A A 933
RLUCVER1.SEQ G A A G A A C G A G C A G 933
RLUCVER2.SEQ G A A G A A C G A G C A G 933
RLUCFINL.SEQ G A A G A A C G A G C A G 933

FIG. 7 (cont'd)

```
RELLUC.SEQ   MTSKVYDPEQRKRMITGPQWWARCKQMNVLDSFINYYDSE 118
RLUCVER1.SEQMASKVYDPEQRKRMITGPQWWARCKQMNVLDSFINYYDSE 118
RLUCVER2.SEQMASKVYDPEQRKRMITGPQWWARCKQMNVLDSFINYYDSE 118
RLUCFINL.SEQMASKVYDPEQRKRMITGPQWWARCKQMNVLDSFINYYDSE 118

RELLUC.SEQ   KHAENAVIFLHGNAASSYLWRHVVPHIEPVARCIIPDLIG 238
RLUCVER1.SEQKHAENAVIFLHGNAASSYLWRHVVPHIEPVARCIIPDLIG 238
RLUCVER2.SEQKHAENAVIFLHGNAASSYLWRHVVPHIEPVARCIIPDLIG 238
RLUCFINL.SEQKHAENAVIFLHGNAASSYLWRHVVPHIEPVARCIIPDLIG 238

RELLUC.SEQ   MGKSGKSGNGSYRLLDHYKYLTAWFELLNLPKKIIFVGHD 358
RLUCVER1.SEQMGKSGKSGNGSYRLLDHYKYLTAWFELLNLPKKIIFVGHD 358
RLUCVER2.SEQMGKSGKSGNGSYRLLDHYKYLTAWFELLNLPKKIIFVGHD 358
RLUCFINL.SEQMGKSGKSGNGSYRLLDHYKYLTAWFELLNLPKKIIFVGHD 358

RELLUC.SEQ   WGACLAFHYSYEHQDKIKAIVHAESVVDVIESWDEWPDIE 478
RLUCVER1.SEQWGACLAFHYSYEHQDKIKAIVHAESVVDVIESWDEWPDIE 478
RLUCVER2.SEQWGACLAFHYSYEHQDKIKAIVHAESVVDVIESWDEWPDIE 478
RLUCFINL.SEQWGACLAFHYSYEHQDKIKAIVHAESVVDVIESWDEWPDIE 478

RELLUC.SEQ   EDIALIKSEEGEKMVLENNFFVETMLPSKIMRKLEPEEFA 598
RLUCVER1.SEQ EDIALIKSEEGEKMVLENNFFVETMLPSKIMRKLEPEEFA 598
RLUCVER2.SEQ EDIALIKSEEGEKMVLENNFFVETMLPSKIMRKLEPEEFA 598
RLUCFINL.SEQ EDIALIKSEEGEKMVLENNFFVETMLPSKIMRKLEPEEFA 598

RELLUC.SEQ   AYLEPFKEKGEVRRPTLSWPREIPLVKGGKPDVVQIVRNY 718
RLUCVER1.SEQ AYLEPFKEKGEVRRPTLSWPREIPLVKGGKPDVVQIVRNY 718
RLUCVER2.SEQ AYLEPFKEKGEVRRPTLSWPREIPLVKGGKPDVVQIVRNY 718
RLUCFINL.SEQ AYLEPFKEKGEVRRPTLSWPREIPLVKGGKPDVVQIVRNY 718

RELLUC.SEQ   NAYLRASDDLPKMFIESDPGFFSNAIVEGAKKFPNTEFVK 838
RLUCVER1.SEQ NAYLRASDDLPKMFIESDPGFFSNAIVEGAKKFPNTEFVK 838
RLUCVER2.SEQ NAYLRASDDLPKMFIESDPGFFSNAIVEGAKKFPNTEFVK 838
RLUCFINL.SEQ NAYLRASDDLPKMFIESDPGFFSNAIVEGAKKFPNTEFVK 838

RELLUC.SEQ   VKGLHFSQEDAPDEMGKYIKSFVERVLKNEQ          931
RLUCVER1.SEQ VKGLHFSQEDAPDEMGKYIKSFVERVLKNEQ          931
RLUCVER2.SEQ VKGLHFSQEDAPDEMGKYIKSFVERVLKNEQ          931
RLUCFINL.SEQ VKGLHFSQEDAPDEMGKYIKSFVERVLKNEQ          931
```

FIG. 8

```
GRVER51.SEQ  ATGATGAAACGCGAAAAGAACGTGATCTACGGCCCAGAAC  40
LUCPPLYG.SEQATGATGAAGAGAGAGAAAAATGTTATATATGGACCCGAAC  40
RD1561H9.SEQATGATAAAGCGTGAGAAAAATGTCATCTATGGCCCTGAGC  40

GRVER51.SEQ  CACTGCATCCACTGGAAGACCTCACCGCTGGTGAGATGCT  80
LUCPPLYG.SEQCCCTACACCCCTTGGAAGACTTAACAGCAGGAGAAATGCT  80
RD1561H9.SEQCTCTCCATCCCTTTGGAGGATTTGACTGCCGGCGAAATGCT  80

GRVER51.SEQ  CTTCCGAGCACTGCGGTAAACATAGTCACCTCCCTCAAGCA 120
LUCPPLYG.SEQCTTCAGGGCCCTTCGAAAACATTCTCATTTACCGCAGGCT 120
RD1561H9.SEQGTTTCGTGCTCTCCGCAAGCACTCTCATTTGCCTCAAGCC 120

GRVER51.SEQ  CTCGTGGACGTCGTGGGAGACGAGAGCCTCTCCTACAAAG 160
LUCPPLYG.SEQTTAGTAGATGTGTTTGGTGACGAATCGCTTTCCTATAAAG 160
RD1561H9.SEQTTGGTCGATGTGGTCGGCGATGAATCTTTGAGCTACAAGG 160

GRVER51.SEQ  AATTTTTCGAAGCTACTGTGCTGTTGGCCCAAAGCCTCCA 200
LUCPPLYG.SEQAGTTTTTTTGAAGCTACATGCCTCCTAGCGCAAAGTCTCCA 200
RD1561H9.SEQAGTTTTTTTGAGGCAACCGTCTTGCTGGCTCAGTCCCTCCA 200

GRVER51.SEQ  TAATTGTGGGTACAAAATGAACGATGTGGTGAGCATTTGT 240
LUCPPLYG.SEQCAATTGTGGATACAAGATGAATGATGTAGTGTCGATCTGC 240
RD1561H9.SEQ CAATTGTGGCTACAAGATGAACGACGTCGTTAGTATCTGT 240

GRVER51.SEQ  GCTGAGAATAACACTCGCTTCTTTATTCCTGTAATCGCCTG 280
LUCPPLYG.SEQ GCCGAGAATAATAAAAGATTTTTTATTCCCATTATTGCAG 280
RD1561H9.SEQ GCTGAAAACAATACCCGTTTCTTCATTCCAGTCATCGCCG 280

GRVER51.SEQ  CTTGGTACATCGGCATGATTGTCGCCCCTGTGAATGAATC 320
LUCPPLYG.SEQ CTTGGTATATTGGTATGATTGTAGCACCTGTTAATGAAAG 320
RD1561H9.SEQ CATGGTATATCGGTATGATCGTGGCTCCAGTCAACGAGAG 320

GRVER51.SEQ  TTACATCCCAGATGAGCTGTGTAAGGTTATGGGTATTAGC 360
LUCPPLYG.SEQTTACATCCCAGATGAACTCTGTAAGGTCATGGGTATATCG 360
RD1561H9.SEQ CTACATTCCCGACGAACTGTGTAAAGTCATGGGTATCTCT 360

GRVER51.SEQ  AAACCTCAAATCGTCTTTACTACCAAAAACATCTTGAATA 400
LUCPPLYG.SEQ AAACCACAAATAGTTTTTTGTACAAAGAACATTTTAAATA 400
RD1561H9.SEQ AAGCCACAGATTGTCTTCACCACTAAGAATATTCTGAACA 400

GRVER51.SEQ  AGGTCTTGGAAGTCCAGTCTCGTACTAACTTCATCAAACG 440
LUCPPLYG.SEQAGGTATTGGAGGTACAGAGCAGAACTAATTTCATAAAAAG 440
RD1561H9.SEQAAGTCCTGGAAGTCCAAAGCCGCACCAACTTTATTAAGCG 440

GRVER51.SEQ  CATCATATTCTGGATACCGTCGAAAACATCCACGGCTGT 480
LUCPPLYG.SEQGATCATCATACTTGATACTGTAGAAAACATACACGGTTGT 480
RD1561H9.SEQTATCATCATCTTGGACACTGTGGAGAATATTCACGGTTGC 480

GRVER51.SEQ  GAGAGCCTCCCCTAACTTCATCTCTCGTTACAGCGATGGTA 520
LUCPPLYG.SEQGAAAGTCTTCCCAATTTTATTTCTCGTTATTCGGATGGAA 520
RD1561H9.SEQGAATCTTTGCCTAATTTCATCTCTCGCTATTCAGACGGCA 520

GRVER51.SEQ  ATATCGCTAATTTCAAGCCCTTGCATTTTGATCCAGTCGA 560
LUCPPLYG.SEQATATTGCCAACTTCAAACCTTTACATTACGATCCTGTTGA 560
RD1561H9.SEQACATCGCAAACTTTAAACCACTCCACTTCGACCCTGTGGA 560
```

FIG. 11

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GRVER51.SEQ  GCAAGTGGCAGCTATTTTGTGCTCCTCCGGCACCACTGGT  600
LUCPPLYG.SEQGCAAGTGGCAGCTATCTTATGTTCGTCAGGCACTACTGGA  600
RD1561H9.SEQACAAGTTGCAGCCATTCTGTGTAGCAGCGGTACTACTGGA  600

GRVER51.SEQ  TTGCCTAAAGGTGTCATGCAGACTCACCAGAATATCTGTG  640
LUCPPLYG.SEQTTACCGAAAGGTGTAATGCAAACTCACCAAAATATTTGTG  640
RD1561H9.SEQCTCCCAAAGGGAGTCATGCAGACCCATCAAAACATTTGCG  640

GRVER51.SEQ  TGCGTTTGATCCACGCCTCTCGACCCTCGTGTGGGTACTCA  680
LUCPPLYG.SEQTCCGACTTATACATGCTTTAGACCCCAGGGCAGGAACGCA  680
RD1561H9.SEQTGCGTCTGATCCATGCCTCTCGATCCACGCTACGGGCACTCA  680

GRVER51.SEQ  ATTGATCCCTGGCGTGACTGTGCTGGTGTATCTGCCTTTC  720
LUCPPLYG.SEQACTTATTCCTGGTGTGACAGTCTTAGTATATCTGCCTTTT  720
RD1561H9.SEQGCTGATTCCTGGTGTCACCGTCTTGGTCTACTTGCCTTTC  720

GRVER51.SEQ  TTTCACGCCTTTGGTTCTCTATTACCCTGGGCTATTTCA  760
LUCPPLYG.SEQTTCCATGCTTTTGGGTTCTCTATAAACTTGGGATACTTCA  760
RD1561H9.SEQTTCCATGCTTTCGGCTTTCATATTACTTGGGTTACTTTA  760

GRVER51.SEQ  TGGTCGGCTTGCGTGTCATCATGTTTCGTCGCTTCGACCA  800
LUCPPLYG.SEQTGGTGGGTCTTCGTGTTATCATGTTAAGACGATTTGATCA  800
RD1561H9.SEQTGGTCGGTCTCCGCGGTGATTATGTTCCGCCGTTTTGATCA  800

GRVER51.SEQ  AGAAGCCTTCTTGAAGGCTATTCAAGACTACGAGGTGCGT  840
LUCPPLYG.SEQAGAAGCATTTCTAAAAGCTATTCAGGATTATGAAGTTCGA  840
RD1561H9.SEQGGAGGCTTTCTTGAAAGCCATCCAAGATTATGAAGTCCGC  840

GRVER51.SEQ  TCCGTGATCAACGTCCCTTCAGTCATTTGTTCCTGAGCA  880
LUCPPLYG.SEQAGTGTAATTAACGTTCCAGCAATAATATTGTTCTTATCGA  880
RD1561H9.SEQAGTGTCATCAACGTGCCTAGCGTGATCCTGTTTTTGTCTA  880

GRVER51.SEQ  AATCTCCTTTGGTTGACAAGTATGATCTGAGCAGCTTGCG  920
LUCPPLYG.SEQAAAGTCCTTTGGTTGACAAATACGATTTATCAAGTTTAAG  920
RD1561H9.SEQAGAGCCCACTCGTGGACAAGTACGACTTGTCTTCACTGCG  920

GRVER51.SEQ  TGAGCTGTGCTGTGGCGCTGCTCCTTGGCCAAAGAAGTG  960
LUCPPLYG.SEQGGAATTGTGTTGCGGTGCGGCACCATTAGCAAAAGAAGTT  960
RD1561H9.SEQTGAATTGTGTTGCGGTGCCGCTCCACTGGCTAAGGAGGTC  960

GRVER51.SEQ  GCCGAGGTCGCTGCTAAGCGTCTGAACCTCCCCTGGTATCC  1000
LUCPPLYG.SEQGCTGAGGTTGCAGTAAAACGATTAAACTTGCCAGGAATTC  1000
RD1561H9.SEQGCTGAAGTGGCCGCCAAACGCTTGAATCTTCCAGGGATTC  1000

GRVER51.SEQ  GCTGCGGTTTTGGTTTGACTGAGAGCACTTCTGCTAACAT  1040
LUCPPLYG.SEQGCTGTGGATTTGGTTTGACAGAATCTACTTCAGCTAATAT  1040
RD1561H9.SEQGTTGTGGCTTCGGCCTCACCGAATCTACCAGTGCGATTAT  1040

GRVER51.SEQ  CCATAGCTTGCGAGACGAGTTTAAGTCTGGTAGCCTGGGT  1080
LUCPPLYG.SEQACACAGTCTTGGGGATGAATTTAAATCAGGATCACTTGGA  1080
RD1561H9.SEQCCAGACTCTCGGGGATGAGTTTAAGAGCGGCTCTTGGGC  1080

GRVER51.SEQ  CGCGTGACTCCTCTTATGGCTGCAAAGATCGCCGACCGTG  1120
LUCPPLYG.SEQAGAGTTACTCCTTTAATGGCAGCTAAAATAGCAGATAGGG  1120
RD1561H9.SEQCGTGTCACTCCACTCATGGCTGCTAAGATCGCTGATCGCG  1120
```

FIG. 11 (cont'd)

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GRVER51.SEQ AGACCGGCAAAAGCACCTGGGCCCAAATCAAGTCGGTGAATT 1160
LUCPPLYG.SEQAAACTGGTAAAGCATTGGGACCAAATCAAGTTGGTGAATT 1160
RD1561H9.SEQAAACTGGTAAGGCTTTGGGCCCGAACCAAGTGGGCGAGCT 1160

GRVER51.SEQ GTGTATTAAGGGCCCTATGGTCTCTAAAGGCTACGTGAAC 1200
LUCPPLYG.SEQATGCGTTAAAGGTCCCATGGTATCGAAAGGTTACGTGAAC 1200
RD1561H9.SEQGTGTATCAAAGGCCCTATGGTGAGCAAGGGTTATGTCAAT 1200

GRVER51.SEQ AATGTGGAGGCCACTAAAGAAGCCATTGATGATGATGGCT 1240
LUCPPLYG.SEQAATGTAGAAGCTACCAAAGAAGCTATTGATGATGATGGTT 1240
RD1561H9.SEQAACGTTGAAGCTACCAAGGAGGCCATCGACGACGACGCT 1240

GRVER51.SEQ GGCTCCATAGCGGCGACTTCGGTTACTATGATGAGGACGA 1280
LUCPPLYG.SEQGGCTTCACTCTGGAGACTTTGGATACTATGATGAGGATGA 1280
RD1561H9.SEQGGTTGCATTCTGGTGATTTTGGATATTACGACGAAGATGA 1280

GRVER51.SEQ ACACTTCTATGTGGTCGATCGCTACAAAGAATTGATTAAG 1320
LUCPPLYG.SEQGCATTTCTATGTGGTGGACCGTTACAAGGAATTGATTAAA 1320
RD1561H9.SEQGCATTTTTACGTCGTGGATCGTTACAAGGAGCTGATCAAA 1320

GRVER51.SEQ TACAAAGGCTCTCAAGTCGCACCAGCCGAACTGGAAGAAA 1360
LUCPPLYG.SEQTATAAGGGCTCTCAGGTAGCACCTGCAGAACTAGAAGAGA 1360
RD1561H9.SEQTACAAGGGTAGCCAGGTTGCTCCAGCTGAGTTGGAGAGA 1360

GRVER51.SEQ TTTTGCTGAAGAACCCTTGTATCCGCGACGTGGCCGTCGT 1400
LUCPPLYG.SEQTTTTATTGAAAAATCCATGTATCAGAGATGTTGCTGTGGT 1400
RD1561H9.SEQTTCTGTTGAAAAATCCATGCATTCGCGATGTCGCTGTGGT 1400

GRVER51.SEQ GGGTATCCCAGACTTGGAAGCTGGCGAGTTGCCTAGCGCC 1440
LUCPPLYG.SEQTGGTATTCCTGATCTAGAAGCTGGAGAACTGCCATCTGCG 1440
RD1561H9.SEQCGGCATTCCTGATCTGGAGGCCGGCGAACTGCCCTTCTGCT 1440

GRVER51.SEQ TTTGTGGTGAAACAACCCGGCAAGGAGATCACCTGCTAAGG 1480
LUCPPLYG.SEQTTTGTGGTTAAACAGCCCGGAAAGGAGATTACAGCTAAAG 1480
RD1561H9.SEQTTCGTTGTCAAGCAGCCTGGTACAGAATTACCGCCAAAG 1480

GRVER51.SEQ AGGTCTACGACTATTTGGCCGAGCGCGTGTCTCACACCAA 1520
LUCPPLYG.SEQAAGTGTACGATTATCTTGCCGAGAGGGTCTCCCATACAAA 1520
RD1561H9.SEQAAGTGTATGATTACCTGGCCTGAACGTGTGAGCCATACTAA 1520

GRVER51.SEQ ATATCTGCGTGGCGGCGTCCGCTTCGTCGATTCTATTCCA 1560
LUCPPLYG.SEQGTATTTGCGTGGAGGGGTTCGATTCGTTGATAGCATACCA 1560
RD1561H9.SEQGTACTTGCGTGGCGGCGTGCGTTTTGTTGACTCCATCCCT 1560

GRVER51.SEQ CGCAACGTTACCGGTAAGATCACTCGTAAAGAGTTGCTGA 1600
LUCPPLYG.SEQAGGAATGTTACAGGTAAAATTACAAGAAAGGAACTTCTGA 1600
RD1561H9.SEQCGTAACGTAACAGGCAAAATTACCGCAAGGAGCTGTTGA 1600

GRVER51.SEQ AGCAACTCCTCGAAAAGCTGGCGGC 1626
LUCPPLYG.SEQAGCAGTTGCTGGAGAAGAGTTCTAAACTT 1629
RD1561H9.SEQAACAATTGTTGGTGAAGGCCGGCGGT 1626
```

FIG. 11 (cont'd)

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GRVER51.SEQ MMKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPQA 118
LUCPPLYG.SEQMMKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPQA 118
RD1561H9.SEQMIKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPQA 118

GRVER51.SEQ LVDVVGDESLSYKEFFEATVLLAQSLHNCGYKMNDVVSIC 238
LUCPPLYG.SEQLVDVFGDESLSYKEFFEATCLLAQSLHNCGYKMNDVVSIC 238
RD1561H9.SEQLVDVVGDESLSYKEFFEATVLLAQSLHNCGYKMNDVVSIC 238

GRVER51.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMGIS 358
LUCPPLYG.SEQAENNKRFFIPIIAAWYIGMIVAPVNESYIPDELCKVMGIS 358
RD1561H9.SEQAENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMGIS 358

GRVER51.SEQ KPQIVFTTKNILNKVLEVQSRTNFIKRIIILDTVENIHGC 478
LUCPPLYG.SEQKPQIVFCTKNILNKVLEVQSRTNFIKRIIILDTVENIHGC 478
RD1561H9.SEQKPQIVFTTKNILNKVLEVQSRTNFIKRIIILDTVENIHGC 478

GRVER51.SEQ ESLPNFISRYSDGNIANFKPLHFDPVEQVAAILCSSGTTG 598
LUCPPLYG.SEQESLPNFISRYSDGNIANFKPLHYDPVEQVAAILCSSGTTG 598
RD1561H9.SEQESLPNFISRYSDGNIANFKPLHFDPVEQVAAILCSSGTTG 598

GRVER51.SEQ LPKGVMQTHQNICVRLIHALDPRVGTQLIPGVTVLVYLPF 718
LUCPPLYG.SEQLPKGVMQTHQNICVRLIHALDPRAGTQLIPGVTVLVYLPF 718
RD1561H9.SEQLPKGVMQTHQNICVRLIHALDPRYGTQLIPGVTVLVYLPF 718

GRVER51.SEQ FHAFGFSITLGYFMVGLRVIMFRRFDQEAFLKAIQDYEVR 838
LUCPPLYG.SEQ FHAFGFSINLGYFMVGLRVIMLRRFDQEAFLKAIQDYEVR 838
RD1561H9.SEQ FHAFGFHITLGYFMVGLRVIMFRRFDQEAFLKAIQDYEVR 838

GRVER51.SEQ SVINVPSVILFLSKSPLVDKYDLSSLRELCCGAAPLAKEV 958
LUCPPLYG.SEQ SVINVPAIILFLSKSPLVDKYDLSSLRELCCGAAPLAKEV 958
RD1561H9.SEQ SVINVPSVILFLSKSPLVDKYDLSSLRELCCGAAPLAKEV 958

GRVER51.SEQ AEVAAKRLNLPGIRCGFGLTESTSANIHSLRDEFKSGSLG 1078
LUCPPLYG.SEQ AEVAVKRLNLPGIRCGFGLTESTSANIHSLGDEFKSGSLG 1078
RD1561H9.SEQ AEVAAKRLNLPGIRCGFGLTESTSAIIQTLGDEFKSGSLG 1078

GRVER51.SEQ RVTPLMAAKIADRETGKALGPNQVGELCIKGPMVSKGYVN 1198
LUCPPLYG.SEQ RVTPLMAAKIADRETGKALGPNQVGELCVKGPMVSKGYVN 1198
RD1561H9.SEQ RVTPLMAAKIADRETGKALGPNQVGELCIKGPMVSKGYVN 1198

GRVER51.SEQ NVEATKEAIDDDGWLHSGDFGYYDEDEHFYVVDRYKELIK 1318
LUCPPLYG.SEQNVEATKEAIDDDGWLHSGDFGYYDEDEHFYVVDRYKELIK 1318
RD1561H9.SEQNVEATKEAIDDDGWLHSGDFGYYDEDEHFYVVDRYKELIK 1318

GRVER51.SEQ YKGSQVAPAELEEILLKNPCIRDVAVVGIPDLEAGELPSA 1438
LUCPPLYG.SEQYKGSQVAPAELEEILLKNPCIRDVAVVGIPDLEAGELPSA 1438
RD1561H9.SEQYKGSQVAPAELEEILLKNPCIRDVAVVGIPDLEAGELPSA 1438

GRVER51.SEQ FVVKQPGKEITAKEVYDYLAERVSHTKYLRGGVRFVDSIP 1558
LUCPPLYG.SEQFVVKQPGKEITAKEVYDYLAERVSHTKYLRGGVRFVDSIP 1558
RD1561H9.SEQFVVKQPGTEITAKEVYDYLAERVSHTKYLRGGVRFVDSIP 1558

GRVER51.SEQ RNVTGKITRKELLKQLLEKAGG                    1624
LUCPPLYG.SEQRNVTGKITRKELLKQLLEKSSKL                  1627
RD1561H9.SEQRNVTGKITRKELLKQLLVKAGG                   1624
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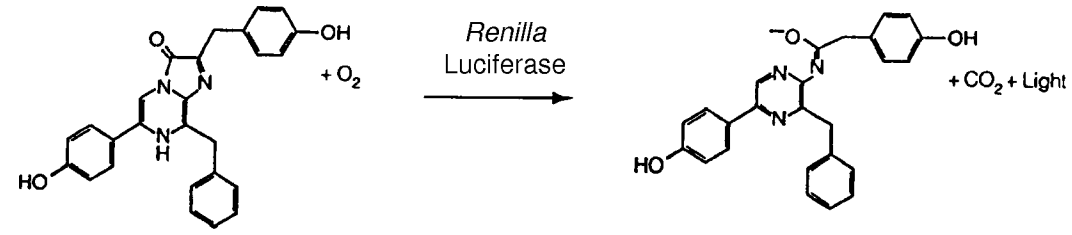
FIG. 12



Coelenterazine

Coelenteramide

FIG. 17B

GRver5.1 DNA sequence of pGL3 vectors

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ATGGTGAAACGCGAAAAGAACGTGATCTACGGCCCAGAACCACTGCATCC   50
ACTGGAAGACCTCACCGCTGGTGAGATGCTCTTCCGAGCACTGCGTAAAC  100
ATAGTCACCTCCCTCAAGCACTCGTGGACGTCGTGGGAGACGAGAgCCTC  150
TCCTACAAAGAATTTTTCGAAGCTACTGTGCTGTTGGCCCAAAGCCTCCA  200
TAATTGTGGGTACAAAATGAACGATGTGGTGAGCATTTGTGCTGAGAATA  250
ACACTCGCTTCTTTATTCCTGTAATCGCTGCTTGGTACATCGGCATGATT  300
GTCGCCCCTGTGAATGAATCTTACATCCCAGATGAGCTGTGTAAGGTTAT  350
GGGTATTAGCAAACCTCAAATCGTCTTTACTACCAAAAACATCTTGAATA  400
AGGTCTTGGAAGTCCAGTCTCGTACTAACTTCATCAAACGCATCATTATT  450
CTGGATACCGTCGAAAACATCCACGGCTGTGAGAGCCTCCCTAACTTCAT  500
CTCTCGTTACAGCGATGGTAATATCGCTAATTTCAAGCCCTTGCATTTTG  550
ATCCAGTCGAGCAAGTGGCCGCTATTTTGTGCTCCTCCGGCACCACTGGT  600
TTGCCTAAAGGTGTCATGCAGACTCACCAGAATATCTGTGTGCGTTTGAT  650
CCACGCTCTCGACCCTCGTGTGGGTACTCAATTGATCcCTGGCGTGACTG  700
TGCTGGTGTATCTGCCTTTCTTTCACGCCTTTGGTTTCTCTATTACCCTG  750
GGCTATTTCATGGTCGGCTTGCGTGTCATCATGTTTCGTCGCTTCGACCA  800
AGAAGCCTTCTTGAAGGCTATTCAAGACTACGAGGTGCGTTCCGTGATCA  850
ACGTCCCTTCAGTCATTTTGTTCCTGAGCAAATCTCCTTTGGTTGACAAG  900
TATGATCTGAGCAGCTTGCGTGAGCTGTGCTGTGGCGCTGCTCCTTTGGC  950
CAAAGAAGTGGCCGAGGTCGCTGCTAAGCGTCTGAACCTCCCTGGTATCC 1000
GCTGCGGTTTTGGTTTGACTGAGAGCACTTCTGCTAACATCCATAGCTTG 1050
CGAGACGAGTTTAAGTCTGGTAGCCTGGGTCGCGTGACTCCTCTTATGGC 1100
TGCAAAGATCGCCGACCGTGAGACCGGCAAAGCACTGGGCCCAAATCAAG 1150
TCGGTGAATTGTGTATTAAGGGCCCTATGGTCTCTAAAGGCTACGTGAAC 1200
AATGTGGAGGCCACTAAAGAAGCCATTGATGATGATGGCTGGCTCCATAG 1250
CGGCGACTTCGGTTACTATGATGAGGACGAACACTTCTATGTGGTCGATC 1300
GCTACAAAGAATTGATTAAGTACAAAGGCTCTCAAGTCGCACCAGCCGAA 1350
CTGGAAGAAATTTTGCTGAAGAACCCTTGTATCCGCGACGTGGCCGTCGT 1400
GGGTATCCCAGACTTGGAAGCTGGCGAGTTGCCTAGCGCCTTTGTGGTGA 1450
AACAACCCGGCAAGGAGATCACTGCTAAGGAGGTCTACGACTATTTGGCC 1500
GAGCGCGTGTCTCACACCAAATATCTGCGTGGCGGCGTCCGCTTCGTCGA 1550
TTCTATTCCACGCAACGTTACCGGTAAGATCACTCGTAAAGAGTTGCTGA 1600
AGCAACTCCTCGAAAAAGCTGGCGGC                          1626
```

SEQ ID NO: 297

FIG. 18A

RDver5.1 DNA sequence of pGL3 vectors

```
ATGGTGAAGCGTGAGAAAAATGTCATCTATGGCCCTGAGCCTCTCCATCC   50
TTTGGAGGATTTGACTGCCGGCGAAATGCTGTTTCGTGCTCTCCGCAAGC  100
ACTCTcATTTGCCTCAAGCCTTGGTCGATGTGGTCGGCGATGAATCTTTG  150
AGCTACAAGGAGTTTTTTGAGGCAACCGTCTTGCTGGCTCAGTCCCTCCA  200
CAATTGTGGCTACAAGATGAACGACGTCGTTAGTATCTGTGCTGAAAACA  250
ATACCCGTTTCTTCATTCCAGTCATCGCCGCATGGTATATCGGTATGATC  300
GTGGCTCCAGTCAACGAGAGCTACATTCCCGACGAACTGTGTAAAGTCAT  350
GGGTATCTCTAAGCCACAGATTGTCTTCACCACTAAGAATATTCTGAACA  400
AAGTCCTGGAAGTCCAAAGCCGCACCAACTTTATTAAGCGTATCATCATC  450
TTGGACACTGTGGAGAATATTCACGGTTGCGAATCTTTGCCTAATTTCAT  500
CTCTCGCTATTCAGACGGCAACATCGCAAACTTTAAACCACTCCACTTCG  550
ACCCTGTGGAACAAGTTGCAGCCATTCTGTGTAGCAGCGGTACTACTGGA  600
CTCCCAAAGGGAGTCATGCAGACCCATCAAAACATTTGCGTGCGTCTGAT  650
CCATGCTCTCGATCCACGCTACGGCACTCAGCTGATTCCTGGTGTCACCG  700
TCTTGGTCTACTTGCCTTTCTTCCATGCTTTCGGCTTTCATATTACTTTG  750
GGTTACTTTATGGTCGGTCTCCGCGTGATTATGTTCCGCCGTTTTGATCA  800
GGAGGCTTTCTTGAAAGCCATCCAAGATTATGAAGTCCGCAGTGTCATCA  850
ACGTGCCTAGCGTGATCCTGTTTTTGTCTAAGAGCCCACTCGTGGACAAG  900
TACGACTTGTCTTCACTGCGTGAATTGTGTTGCGGTGCCGCTCCACTGGC  950
TAAGGAGGTCGCTGAAGTGGCCGCCAAACGCTTGAATCTTCCAGGGATTC 1000
GTTGTGGCTTCGGCCTCACCGAATCTACCAGCGCTATTATTCAGTCTCTC 1050
CGCGATGAGTTTAAGAGCGGCTCTTTGGGCCGTGTCACTCCACTCATGGC 1100
TGCTAAGATCGCTGATCGCGAAACTGGTAAGGCTTTGGGCCCGAACCAAG 1150
TGGGCGAGCTGTGTATCAAAGGCCCTATGGTGAGCAAGGGTTATGTCAAT 1200
AACGTTGAAGCTACCAAGGAGGCCATCGACGACGACGGCTGGTTGCATTC 1250
TGGTGATTTTGGATATTACGACGAAGATGAGCATTTTTACGTCGTGGATC 1300
GTTACAAGGAGCTGATCAAATACAAGGGTAGCCAGGTTGCTCCAGCTGAG 1350
TTGGAGGAGATTCTGTTGAAAAATCCATGCATTCGCGATGTCGCTGTGGT 1400
CGGCATTCCTGATCTGGAGGCCGGCGAACTGCCTTCTGCTTTCGTTGTCA 1450
AGCAGCCTGGTAAAGAAATTACCGCCAAAGAAGTGTATGATTACCTGGCT 1500
GAACGTGTGAGCCATACTAAGTACTTGCGTGGCGGCGTGCGTTTTGTTGA 1550
CTCCATCCCTCGTAACGTAACAGGCAAAATTACCCGCAAGGAGCTGTTGA 1600
AACAATTGTTGGAGAAGGCCGGCGGT                          1626
```

SEQ ID NO: 299

FIG. 18A (cont'd)

RD1561H9 DNA sequenc of pGL3 vectors

```
ATGGTAAAGCGTGAGAAAAATGTCATCTATGGCCCTGAGCCTCTCCATCC   50
TTTGGAGGATTTGACTGCCGGCGAAATGCTGTTTCGTGCTCTCCGCAAGC  100
ACTCTCATTTGCCTCAAGCCTTGGTCGATGTGGTCGGCGATGAATCTTTG  150
AGCTACAAGGAGTTTTTTGAGGCAACCGTCTTGCTGGCTCAGTCCCTCCA  200
CAATTGTGGCTACAAGATGAACGACGTCGTTAGTATCTGTGCTGAAAACA  250
ATACCCGTTTCTTCATTCCAGTCATCGCCGCATGGTATATCGGTATGATC  300
GTGGCTCCAGTCAACGAGAGCTACATTCCCGACGAACTGTGTAAAGTCAT  350
GGGTATCTCTAAGCCACAGATTGTCTTCACCACTAAGAATATTCTGAACA  400
AAGTCCTGGAAGTCCAAAGCCGCACCAACTTTATTAAGCGTATCATCATC  450
TTGGACACTGTGGAGAATATTCACGGTTGCGAATCTTTGCCTAATTTCAT  500
CTCTCGCTATTCAGACGGCAACATCGCAAACTTTAAACCACTCCACTTCG  550
ACCCTGTGGAACAAGTTGCAGCCATTCTGTGTAGCAGCGGTACTACTGGA  600
CTCCCAAAGGGAGTCATGCAGACCCATCAAAACATTTGCGTGCGTCTGAT  650
CCATGCTCTCGATCCACGCTACGGCACTCAGCTGATTCCTGGTGTCACCG  700
TCTTGGTCTACTTGCCTTTCTTCCATGCTTTCGGCTTTCATATTACTTTG  750
GGTTACTTTATGGTCGGTCTCCGCGTGATTATGTTCCGCCGTTTTGATCA  800
GGAGGCTTTCTTGAAAGCCATCCAAGATTATGAAGTCCGCAGTGTCATCA  850
ACGTGCCTAGCGTGATCCTGTTTTTGTCTAAGAGCCCACTCGTGGACAAG  900
TACGACTTGTCTTCACTGCGTGAATTGTGTTGCGGTGCCGCTCCACTGGC  950
TAAGGAGGTCGCTGAAGTGGCCGCCAAACGCTTGAATCTTCCAGGGATTC 1000
GTTGTGGCTTCGGCCTCACCGAATCTACCAGTGCGATTATCCAGACTCTC 1050
GGGGATGAGTTTAAGAGCGGCTCTTTGGGCCGTGTCACTCCACTCATGGC 1100
TGCTAAGATCGCTGATCGCGAAACTGGTAAGGCTTTGGGCCCGAACCAAG 1150
TGGGCGAGCTGTGTATCAAAGGCCCTATGGTGAGCAAGGGTTATGTCAAT 1200
AACGTTGAAGCTACCAAGGAGGCCATCGACGACGACGGCTGGTTGCATTC 1250
TGGTGATTTTGGATATTACGACGAAGATGAGCATTTTTACGTCGTGGATC 1300
GTTACAAGGAGCTGATCAAATACAAGGGTAGCCAGGTTGCTCCAGCTGAG 1350
TTGGAGGAGATTCTGTTGAAAAATCCATGCATTCGCGATGTCGCTGTGGT 1400
CGGCATTCCTGATCTGGAGGCCGGCGAACTGCCTTCTGCTTTCGTTGTCA 1450
AGCAGCCTGGTACAGAAATTACCGCCAAAGAAGTGTATGATTACCTGGCT 1500
GAACGTGTGAGCCATACTAAGTACTTGCGTGGCGGCGTGCGTTTTGTTGA 1550
CTCCATCCCTCGTAACGTAACAGGCAAAATTACCCGCAAGGAGCTGTTGA 1600
AACAATTGTTGGTGAAGGCCGGCGGT                          1626
```

SEQ ID NO: 301

FIG. 18A (cont'd)

GRver5.1 protein sequence of pGL3 vectors

```
MVKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPQALVDVVGDESL  50
SYKEFFEATVLLAQSLHNCGYKMNDVVSICAENNTRFFIPVIAAWYIGMI 100
VAPVNESYIPDELCKVMGISKPQIVFTTKNILNKVLEVQSRTNFIKRIII 150
LDTVENIHGCESLPNFISRYSDGNIANFKPLHFDPVEQVAAILCSSGTTG 200
LPKGVMQTHQNICVRLIHALDPRVGTQLIPGVTVLVYLPFFHAFGFSITL 250
GYFMVGLRVIMFRRFDQEAFLKAIQDYEVRSVINVPSVILFLSKSPLVDK 300
YDLSSLRELCCGAAPLAKEVAEVAAKRLNLPGIRCGFGLTESTSANIHSL 350
RDEFKSGSLGRVTPLMAAKIADRETGKALGPNQVGELCIKGPMVSKGYVN 400
NVEATKEAIDDDGWLHSGDFGYYDEDEHFYVVDRYKELIKYKGSQVAPAE 450
LEEILLKNPCIRDVAVVGIPDLEAGELPSAFVVKQPGKEITAKEVYDYLA 500
ERVSHTKYLRGGVRFVDSIPRNVTGKITRKELLKQLLEKAGG          542
```

SEQ ID NO: 298

RDver5.1 protein sequence of pGL3 vectors

```
MVKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPQALVDVVGDESL  50
SYKEFFEATVLLAQSLHNCGYKMNDVVSICAENNTRFFIPVIAAWYIGMI 100
VAPVNESYIPDELCKVMGISKPQIVFTTKNILNKVLEVQSRTNFIKRIII 150
LDTVENIHGCESLPNFISRYSDGNIANFKPLHFDPVEQVAAILCSSGTTG 200
LPKGVMQTHQNICVRLIHALDPRYGTQLIPGVTVLVYLPFFHAFGFHITL 250
GYFMVGLRVIMFRRFDQEAFLKAIQDYEVRSVINVPSVILFLSKSPLVDK 300
YDLSSLRELCCGAAPLAKEVAEVAAKRLNLPGIRCGFGLTESTSAIIQSL 350
RDEFKSGSLGRVTPLMAAKIADRETGKALGPNQVGELCIKGPMVSKGYVN 400
NVEATKEAIDDDGWLHSGDFGYYDEDEHFYVVDRYKELIKYKGSQVAPAE 450
LEEILLKNPCIRDVAVVGIPDLEAGELPSAFVVKQPGKEITAKEVYDYLA 500
ERVSHTKYLRGGVRFVDSIPRNVTGKITRKELLKQLLEKAGG          542
```

SEQ ID NO: 300

RD1561H9 protein sequence of pGL3 vectors

```
MVKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPQALVDVVGDESL  50
SYKEFFEATVLLAQSLHNCGYKMNDVVSICAENNTRFFIPVIAAWYIGMI 100
VAPVNESYIPDELCKVMGISKPQIVFTTKNILNKVLEVQSRTNFIKRIII 150
LDTVENIHGCESLPNFISRYSDGNIANFKPLHFDPVEQVAAILCSSGTTG 200
LPKGVMQTHQNICVRLIHALDPRYGTQLIPGVTVLVYLPFFHAFGFHITL 250
GYFMVGLRVIMFRRFDQEAFLKAIQDYEVRSVINVPSVILFLSKSPLVDK 300
YDLSSLRELCCGAAPLAKEVAEVAAKRLNLPGIRCGFGLTESTSAIIQTL 350
GDEFKSGSLGRVTPLMAAKIADRETGKALGPNQVGELCIKGPMVSKGYVN 400
NVEATKEAIDDDGWLHSGDFGYYDEDEHFYVVDRYKELIKYKGSQVAPAE 450
LEEILLKNPCIRDVAVVGIPDLEAGELPSAFVVKQPGTEITAKEVYDYLA 500
ERVSHTKYLRGGVRFVDSIPRNVTGKITRKELLKQLLVKAGG          542
```

SEQ ID NO: 302

FIG. 18A (cont'd)